

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 22:16:34 ; Search time 136 Seconds
(without alignments)
261.406 Million cell updates/sec

Title: US-10-671-074-172

Perfect score: 20

Sequence: 1 gcttggttggtggcaacacat 20

Scoring table: Oligo NUC

Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 0

Total number of hits satisfying chosen parameters: 428752

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : Issued Patents_NA.*
1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	55.0	16	3 US-08-485-942A-85	Sequence 85, Appl
2	11	55.0	16	3 US-08-488-214A-85	Sequence 85, Appl
3	11	55.0	16	3 US-08-488-208A-85	Sequence 85, Appl
4	11	55.0	16	3 US-08-483-211A-85	Sequence 85, Appl
5	11	55.0	16	3 US-08-488-223A-85	Sequence 85, Appl
6	11	55.0	16	3 US-08-438-431A-85	Sequence 85, Appl
7	11	55.0	16	3 US-08-488-225A-85	Sequence 85, Appl
8	11	55.0	18	3 US-09-255-893-45	Sequence 45, Appl
9	11	55.0	18	3 US-09-255-893-45	Sequence 46, Appl
10	11	55.0	18	3 US-09-344-521-28	Sequence 28, Appl
11	11	55.0	18	3 US-09-422-978-6545	Sequence 6545, Ap
12	11	55.0	19	2 US-08-690-734A-50	Sequence 50, Appl
13	11	55.0	19	3 US-08-742-185-50	Sequence 50, Appl
14	11	55.0	20	2 US-08-531-556-117	Sequence 117, App
15	11	55.0	20	2 US-08-753-979A-19	Sequence 19, Appl
16	11	55.0	20	3 US-09-230-652-72	Sequence 72, Appl
17	11	55.0	20	3 US-09-198-452A-5551	Sequence 5551, Ap
18	10	50.0	16	3 US-09-052-333A-55	Sequence 55, Appl
19	10	50.0	17	2 US-08-234-613-19	Sequence 19, Appl
20	10	50.0	17	2 US-08-484-192-91	Sequence 91, Appl
21	10	50.0	17	2 US-08-237-973-32	Sequence 32, Appl
22	10	50.0	17	3 US-09-333-611-23	Sequence 23, Appl
23	10	50.0	17	3 US-09-474-432B-431	Sequence 431, App
24	10	50.0	17	3 US-09-476-387-430	Sequence 430, App

c	25	10	50.0	18	2	US-08-432-871C-53	Sequence 53, Appl
	26	10	50.0	18	3	US-09-255-893-44	Sequence 44, Appl
	27	10	50.0	18	3	US-09-071-710-23	Sequence 23, Appl
	28	10	50.0	18	3	US-09-525-397-23	Sequence 23, Appl
	29	10	50.0	18	3	US-09-630-706-21	Sequence 21, Appl
c	30	10	50.0	18	3	US-09-270-956-53	Sequence 53, Appl
	31	10	50.0	19	2	US-08-632-575B-17	Sequence 17, Appl
	32	10	50.0	19	3	US-09-199-542B-17	Sequence 17, Appl
c	33	10	50.0	19	3	US-09-422-978-5558	Sequence 5558, Ap
	34	10	50.0	20	3	US-08-832-985-10	Sequence 10, Appl
c	35	10	50.0	20	3	US-09-158-347-4	Sequence 4, Appl
	36	10	50.0	20	3	US-09-425-638A-15	Sequence 15, Appl
	37	10	50.0	20	3	US-09-543-004-15	Sequence 15, Appl
c	38	10	50.0	20	3	US-09-702-251-45	Sequence 45, Appl
	39	10	50.0	20	3	US-09-410-903-70	Sequence 70, Appl
c	40	10	50.0	20	3	US-09-410-903-76	Sequence 76, Appl
c	41	10	50.0	20	3	US-09-410-903-91	Sequence 91, Appl
c	42	10	50.0	20	3	US-09-360-416-129	Sequence 129, App
c	43	10	50.0	20	3	US-08-835-159-10	Sequence 10, Appl
c	44	10	50.0	20	3	US-09-198-452A-2956	Sequence 2956, Ap
	45	10	50.0	20	3	US-09-980-052-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-08-485-942A-85
; Sequence 85, Application US/08485942A
; Patent No. 6048837
; GENERAL INFORMATION:
; APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA,
; APPLICANT: MARGHERITA MAFFEI, JEFFREY HALAAS, KETAN GAJTWALA, AND STEPHEN K. BURR
; TITLE OF INVENTION: OB POLYPEPTIDE AS MODULATORS OF BODY WEIGHT (AS
; TITLE OF INVENTION: AMENDED)
; NUMBER OF SEQUENCES: 99
; CORRESPONDENCE ADDRESS:
; ADDRESS: Klauber & Jackson
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,942A
; FILING DATE: JUNE 7, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6048837ember 30, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 85:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (primer)
; DESCRIPTION: Marker AFM218xf10
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
US-08-488-214A-85

Query Match          55.0%; Score 11; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGGGCAACACA 19
   |||||
Db 1 TGGGCAACACA 11

RESULT 3
US-08-488-208A-85
; Sequence 85, Application US/08488208A
; Patent No. 6124448
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,208A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: 08/485,943
; FILING DATE: June 7, 1995
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6124448ember 30, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP21
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (primer)

```

; DESCRIPTION: Marker AFM218xf10
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
US-08-488-208A-85

Query Match 55.0%; Score 11; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGGGCAACACA 19
| | | | | | | | | |
Db 1 TGGGCAACACA 11

RESULT 4

US-08-483-211A-85
; Sequence 85, Application US/08483211A
; Patent No. 6309853

GENERAL INFORMATION:

; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: USES THEREOF

; NUMBER OF SEQUENCES: 98

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klauber & Jackson

; STREET: 411 Hackensack Avenue

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/483,211A

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/485,943

; FILING DATE: June 7, 1995

; APPLICATION NUMBER: 08/438,431

; FILING DATE: May 10, 1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/347,563

; FILING DATE: No. 6309853ember 30, 1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/292,345

; FILING DATE: August 17, 1994

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Jackson Esq., David A.

; REGISTRATION NUMBER: 26,742

; REFERENCE/DOCKET NUMBER: 600-1-087 CIP21

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201 487-5900

; TELEFAX: 201 343-1684

; TELEX: 133521

; INFORMATION FOR SEQ ID NO: 85:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (primer)

; DESCRIPTION: Marker AFM218xf10

; HYPOTHETICAL: NO

; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
US-08-483-211A-85

Query Match 55.0%; Score 11; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGGGCAACACA 19
| | | | | | | | | |
Db 1 TGGGCAACACA 11

RESULT 5

US-08-488-223A-85

; Sequence 85, Application US/08488223A

; Patent No. 6350730

; GENERAL INFORMATION:

; APPLICANT: THE ROCKEFELLER UNIVERSITY

; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC

; TITLE OF INVENTION: ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES TH

; NUMBER OF SEQUENCES: 98

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klauber & Jackson

; STREET: 411 Hackensack Avenue

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/488,223A

; FILING DATE: 07-Jun-1995

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/485,943

; FILING DATE: <Unknown>

; APPLICATION NUMBER: 08/347,563

; FILING DATE: No. 6350730ember 30, 1994

; APPLICATION NUMBER: 08/292,345

; FILING DATE: August 17, 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Jackson Esq., David A.

; REGISTRATION NUMBER: 26,742

; REFERENCE/DOCKET NUMBER: 600-1-087 CIP21

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201 487-5900

; TELEFAX: 201 343-1684

; TELEX: 133521

; INFORMATION FOR SEQ ID NO: 85:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (primer)

; DESCRIPTION: Marker AFM218xf10

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Human

; SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Query Match 55.0%; Score 11; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Tue Jan 10 10:02:46 2006

us-10-671-074-172.oligo.rni

```
QY      9 TGGGCAACACA 19
Db      1 TGGGCAACACA 11

RESULT 6
US-08-438-431A-85
; Sequence 85, Application US/08438431A
; Patent No. 6429290
; GENERAL INFORMATION:
; APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA, MARGHERITA MAFFEI.
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC ACIDS AND PR
; NUMBER OF SEQUENCES: 99
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,431A
; FILING DATE: May 10, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6429290ember 30, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (primer)
; DESCRIPTION: Marker AFM218xf10
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; US-08-438-431A-85

Query Match      55.0%; Score 11; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 TGGGCAACACA 19
Db      1 TGGGCAACACA 11

RESULT 7
US-08-488-225A-85
; Sequence 85, Application US/08488225A
; Patent No. 6471956
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
```

```
APPLICANT: THE ROCKEFELLER UNIVERSITY
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USE:
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,225A
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/483,211
FILING DATE: June 7, 1995
CLASSIFICATION: 435
APPLICATION DATA:
APPLICATION NUMBER: 08/438,431
FILING DATE: May 10, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/347,563
FILING DATE: No. 6471956ember 30, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/292,345
FILING DATE: August 17, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087 CIP2J
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (primer)
DESCRIPTION: Marker AFM218xf10
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
US-08-488-225A-85

Query Match      55.0%; Score 11; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 TGGGCAACACA 19
Db      1 TGGGCAACACA 11

RESULT 8
US-09-255-893-45
; Sequence 45, Application US/09255893A
; Patent No. 6008344
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
```

; APPLICANT: Lex M. Cowert
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2 GROUP IV EXPRESSION
; FILE REFERENCE: RTS-0055
; CURRENT APPLICATION NUMBER: US/09/255,893A
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 45
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-255-893-45

Query Match 55.0%; Score 11; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGTTGGGCAA 15
| | | | | | | | | |
DB 3 TGGTTGGGCAA 13

RESULT 9
US-09-255-893-46
; Sequence 46, Application US/09255893A
; Patent No. 6008344
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowert
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2 GROUP IV EXPRESSION
; FILE REFERENCE: RTS-0055
; CURRENT APPLICATION NUMBER: US/09/255,893A
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 46
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-255-893-46

Query Match 55.0%; Score 11; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGTTGGGCAA 15
| | | | | | | | | |
DB 6 TGGTTGGGCAA 16

RESULT 10
US-09-344-521-28/c
; Sequence 28, Application US/09344521
; Patent No. 6100990
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowert
; TITLE OF INVENTION: ANTISENSE MODULATION OF PI3K P85 EXPRESSION
; FILE REFERENCE: RTS-0062
; CURRENT APPLICATION NUMBER: US/09/344,521
; CURRENT FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 28
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-344-521-28

Query Match 55.0%; Score 11; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGTTGGGCAA 15
| | | | | | | | | |
DB 11 TGGTTGGGCAA 1

RESULT 11
US-09-422-978-6545
; Sequence 6545, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET 020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6545
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-12224 for SEQ 2611,
US-09-422-978-6545

Query Match 55.0%; Score 11; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGGGCAACA 17
| | | | | | | | | |
DB 4 GTTGGGCAACA 14

RESULT 12
US-08-690-734A-50/c
; Sequence 50, Application US/08690734A
; Patent No. 5871920
; GENERAL INFORMATION:
; APPLICANT: Page, David C.
; APPLICANT: Reijo, Renee
; TITLE OF INVENTION: DAZ: A GENE ASSOCIATED WITH AZOOSPERMIA
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,734A
; FILING DATE: 31-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/310,429

```

; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WH194-07A
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-690-734A-50

Query Match 55.0%; Score 11; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGGCAACACAT 20
DB 15 GGGCAACACAT 5

RESULT 13
US-08-742-185-50/C
; Sequence 50, Application US/08742185
; Patent No. 6020476
; GENERAL INFORMATION:
; APPLICANT: Page, David C.
; APPLICANT: Reijo, Renee
; APPLICANT: Saxena, Richa
; APPLICANT: Hawkins, Trevor
; APPLICANT: Reeve, Mary Pat
; TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,185
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 08/690,734
; FILING DATE: 31-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/310,429
; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WH194-07A2
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-742-185-50

```

```

Query Match 55.0%; Score 11; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGGCAACACAT 20
DB 15 GGGCAACACAT 5

RESULT 14
US-08-531-556-117/c
; Sequence 117, Application US/08531556
; Patent No. 5776882
; GENERAL INFORMATION:
; APPLICANT: Agoulnik, Alexander I
; APPLICANT: Kent First, Marijo
; APPLICANT: Mualllem, Ariege
; TITLE OF INVENTION: MALE INFERTILITY Y-DELETION DETECTION
; TITLE OF INVENTION: BATTERY
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/531.556
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.034CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-831-2100
; TELEFAX: 608-831-2106
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-531-556-117

Query Match 55.0%; Score 11; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGGCAACACAT 20
DB 15 GGGCAACACAT 5

RESULT 15
US-08-753-979A-19/c
; Sequence 19, Application US/08753979A
; Patent No. 5840549
; GENERAL INFORMATION:
; APPLICANT: Kent First, Marijo
; APPLICANT: Mualllem, Ariege
; TITLE OF INVENTION: MALE INFERTILITY Y-DELETION DETECTION
; TITLE OF INVENTION: BATTERY
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: DeWitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: WI
COUNTRY: USA
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/753,979A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 34506.051
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-831-2100
TELEFAX: 608-831-2106
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-753-979A-19

Query Match 55.0%; Score 11; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 GGGCAACACAT 20
Db 15 GGGCAACACAT 5
|||||

Search completed: January 10, 2006, 00:13:28
Job time : 137 secs

Page Blank (up to)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 22:32:34 ; Search time 778 Seconds
(without alignments)
212.580 Million cell updates/sec

Title: US-10-671-074-172

Perfect score: 20

Sequence: 1 gcttgggtgggcaacacat 20

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1817756

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : Published Applications NA Main:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	7 US-10-671-074-172	Sequence 172, Appl
2	19	95.0	20	7 US-10-671-074-40	Sequence 40, Appl
3	19	95.0	20	7 US-10-671-074-118	Sequence 118, Appl
4	16	80.0	20	7 US-10-671-074-41	Sequence 41, Appl
5	16	80.0	20	7 US-10-671-074-119	Sequence 119, Appl
6	14	70.0	20	7 US-10-688-706-95	Sequence 95, Appl
7	14	70.0	20	7 US-10-688-706-125	Sequence 125, Appl
8	14	70.0	20	7 US-10-688-706-141	Sequence 141, Appl
9	14	70.0	20	7 US-10-688-706-170	Sequence 170, Appl
10	14	70.0	20	7 US-10-688-706-273	Sequence 273, Appl
11	14	70.0	20	7 US-10-688-706-695	Sequence 695, Appl
12	14	70.0	20	7 US-10-688-706-727	Sequence 727, Appl
13	13	65.0	20	7 US-10-688-706-444	Sequence 444, Appl
14	13	65.0	20	7 US-10-688-706-1058	Sequence 1058, Ap
15	12	60.0	20	7 US-10-688-706-190	Sequence 190, Appl
16	12	60.0	20	7 US-10-688-706-229	Sequence 229, Appl
17	11	55.0	12	8 US-10-257-017B-276516	Sequence 276516,
18	11	55.0	12	8 US-10-257-017B-330753	Sequence 330753,
19	11	55.0	13	8 US-10-257-017B-209229	Sequence 209229,
20	11	55.0	13	8 US-10-257-017B-209230	Sequence 209230,
21	11	55.0	16	3 US-09-736-084-85	Sequence 85, Appl
22	11	55.0	16	8 US-10-730-488-85	Sequence 85, Appl
23	11	55.0	17	3 US-09-780-164-530	Sequence 530, Appl

ALIGNMENTS

RESULT 1

US-10-671-074-172
; Sequence 172, Application US/10671074
; Publication No. US20040097459A1
; GENERAL INFORMATION:
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Bhanot, Sanjay
; APPLICANT: Veniant-Ellison, Murielle
; APPLICANT: Lindberg, Richard A.
; APPLICANT: Shutter, John R.
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX O1A EXPRESSION
; FILE REFERENCE: AMGN0001-101
; CURRENT APPLICATION NUMBER: US/10/671,074
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: US 10/260,203
; PRIOR FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 172
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-671-074-172

Query Match 100.0%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAACACAT 20
|||||

Db 1 GCTTTGGTTGGCAACACAT 20
|||||

RESULT 2

US-10-671-074-40
; Sequence 40, Application US/10671074
; Publication No. US20040097459A1
; GENERAL INFORMATION:
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Bhanot, Sanjay
; APPLICANT: Veniant-Ellison, Murielle
; APPLICANT: Lindberg, Richard A.
; APPLICANT: Shutter, John R.
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX O1A EXPRESSION
; FILE REFERENCE: AMGN0001-101

Sequence 531, App
Sequence 532, App
Sequence 533, App
Sequence 905, App
Sequence 6545, Ap
Sequence 28, Appl
Sequence 184, App
Sequence 380, App
Sequence 3, Appl
Sequence 77, Appl
Sequence 17, Appl
Sequence 72, Appl
Sequence 5551, Ap
Sequence 101, App
Sequence 305, App
Sequence 88, Appl
Sequence 301, App
Sequence 275412,
Sequence 275681,
Sequence 297223,
Sequence 297227,
Sequence 298160,

us-10-671-074-172.oligo.rnpbm

Tue Jan 10 10:02:47 2006

```
;
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-671-074-41
Query Match      80.0%; Score 16; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAAC 16
Db 5 GCTTTGGTTGGCAAC 20

RESULT 5
US-10-671-074-119/c
; Sequence 119, Application US/10671074
; Publication No. US20040097459A1
; GENERAL INFORMATION:
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Bhanot, Sanjay
; APPLICANT: Veniant-Ellison, Murielle
; APPLICANT: Lindberg, Richard A.
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX O1A EXPRESSION
; FILE REFERENCE: AMGN0001-101
; CURRENT APPLICATION NUMBER: US/10/671,074
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: US 10/260,203
; PRIOR FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-671-074-119
Query Match      80.0%; Score 16; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGCAAC 16
Db 16 GCTTTGGTTGGCAAC 1

RESULT 6
US-10-688-706-95/c
; Sequence 95, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 95
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-95
Query Match      70.0%; Score 14; DB 7; Length 20;
```

```
;
; CURRENT APPLICATION NUMBER: US/10/671,074
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: US 10/260,203
; PRIOR FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-671-074-40
Query Match      95.0%; Score 19; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTTGGTTGGCAACACAT 20
Db 1 CTTTGGTTGGCAACACAT 19

RESULT 3
US-10-671-074-118/c
; Sequence 118, Application US/10671074
; Publication No. US20040097459A1
; GENERAL INFORMATION:
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Bhanot, Sanjay
; APPLICANT: Veniant-Ellison, Murielle
; APPLICANT: Lindberg, Richard A.
; APPLICANT: Shutter, John R.
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX O1A EXPRESSION
; FILE REFERENCE: AMGN0001-101
; CURRENT APPLICATION NUMBER: US/10/671,074
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: US 10/260,203
; PRIOR FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 118
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-671-074-118
Query Match      95.0%; Score 19; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTTGGTTGGCAACACAT 20
Db 20 CTTTGGTTGGCAACACAT 2

RESULT 4
US-10-671-074-41
; Sequence 41, Application US/10671074
; Publication No. US20040097459A1
; GENERAL INFORMATION:
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Bhanot, Sanjay
; APPLICANT: Veniant-Ellison, Murielle
; APPLICANT: Lindberg, Richard A.
; APPLICANT: Shutter, John R.
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX O1A EXPRESSION
; FILE REFERENCE: AMGN0001-101
; CURRENT APPLICATION NUMBER: US/10/671,074
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: US 10/260,203
; PRIOR FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 41
```

```
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 7 GTTGGGCAACACAT 20
Db 18 GTTGGGCAACACAT 5

RESULT 7
US-10-688-706-125/c
; Sequence 125, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Brochat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; PRIOR FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 125
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-125

Query Match 70.0%; Score 14; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGGGCAACACAT 20
Db 20 GTTGGGCAACACAT 7

RESULT 8
US-10-688-706-141/c
; Sequence 141, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Brochat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; PRIOR FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 141
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-141

Query Match 70.0%; Score 14; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGGGCAACACAT 20
Db 19 GTTGGGCAACACAT 6

RESULT 9
US-10-688-706-141/c
; Sequence 141, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Brochat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; PRIOR FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 141
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-141

Query Match 70.0%; Score 14; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGGGCAACACAT 20
Db 16 GTTGGGCAACACAT 3

RESULT 11
US-10-688-706-695/c
; Sequence 695, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Brochat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
```

us-10-671-074-172.oligo.rnpbm

Tue Jan 10 10:02:47 2006

```

; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 695
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-695

Query Match 70.0%; Score 14; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGGGCAACACAT 20
Db 14 GTTGGGCAACACAT 1

RESULT 12
US-10-688-706-727/c
; Sequence 727, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Brochat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 727
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-727

Query Match 70.0%; Score 14; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGGGCAACACAT 20
Db 15 GTTGGGCAACACAT 2

RESULT 13
US-10-688-706-444/c
; Sequence 444, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Brochat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 444
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-444

Query Match 65.0%; Score 13; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGGGCAACACAT 20
Db 20 TTGGGCAACACAT 8

FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-444

Query Match 65.0%; Score 13; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGGGCAACACAT 20
Db 20 TTGGGCAACACAT 8

RESULT 14
US-10-688-706-1058/c
; Sequence 1058, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Brochat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1058
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-1058

Query Match 65.0%; Score 13; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGGGCAACACA 19
Db 13 GTTGGGCAACACA 1

RESULT 15
US-10-688-706-190/c
; Sequence 190, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Brochat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 190
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-190

Query Match 60.0%; Score 12; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGGGCAACACAT 20

```

Db |||||||
 20 TGGCAACACAT 9

Search completed: January 10, 2006, 00:26:41
Job time : 779 secs

ALL INFORMATION CONTAINED
HEREIN IS UNCLASSIFIED
DATE 08-22-2011 BY 60322
UCBAW/BJA

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 22:35:54 ; Search time 320 Seconds
(without alignments)
45.567 Million cell updates/sec

Title: US-10-671-074-172

Perfect score: 20

Sequence: 1 gcttgggtgggcaacacat 20

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4637633 seqs, 364532575 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6446046

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : Published Applications NA New:*

- 1: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	12	60.0	19	8	US-11-101-244-619761
C 2	12	60.0	19	8	US-11-101-244-619858
C 3	12	60.0	19	8	US-11-101-244-1014343
C 4	12	60.0	19	8	US-11-101-244-1536666
C 5	12	60.0	19	9	US-11-083-784-619761
C 6	12	60.0	19	9	US-11-083-784-619858
C 7	12	60.0	19	9	US-11-083-784-1014343
C 8	12	60.0	19	9	US-11-083-784-1536666
C 9	11	55.0	19	8	US-11-101-244-90162
C 10	11	55.0	19	8	US-11-101-244-204871
C 11	11	55.0	19	8	US-11-101-244-341693
C 12	11	55.0	19	8	US-11-101-244-352435
C 13	11	55.0	19	8	US-11-101-244-580035
C 14	11	55.0	19	8	US-11-101-244-676846
C 15	11	55.0	19	8	US-11-101-244-694038
C 16	11	55.0	19	8	US-11-101-244-744106
C 17	11	55.0	19	8	US-11-101-244-1071283
C 18	11	55.0	19	8	US-11-101-244-1104410
C 19	11	55.0	19	8	US-11-101-244-1104472
C 20	11	55.0	19	8	US-11-101-244-1279593
C 21	11	55.0	19	8	US-11-101-244-1280905
C 22	11	55.0	19	8	US-11-101-244-1286934
C 23	11	55.0	19	8	US-11-101-244-1286940

24	11	55.0	19	8	US-11-101-244-132286	Sequence 132286,
25	11	55.0	19	8	US-11-101-244-1343921	Sequence 1343921,
26	11	55.0	19	8	US-11-101-244-1345283	Sequence 1345283,
C 27	11	55.0	19	8	US-11-101-244-1460190	Sequence 1460190,
C 28	11	55.0	19	8	US-11-101-244-1467386	Sequence 1467386,
C 29	11	55.0	19	8	US-11-101-244-1576865	Sequence 1576865,
C 30	11	55.0	19	8	US-11-101-244-1576868	Sequence 1576868,
C 31	11	55.0	19	9	US-11-083-784-90162	Sequence 90162, A
C 32	11	55.0	19	9	US-11-083-784-204871	Sequence 204871,
C 33	11	55.0	19	9	US-11-083-784-341693	Sequence 341693,
C 34	11	55.0	19	9	US-11-083-784-352435	Sequence 352435,
C 35	11	55.0	19	9	US-11-083-784-580035	Sequence 580035,
C 36	11	55.0	19	9	US-11-083-784-676846	Sequence 676846,
C 37	11	55.0	19	9	US-11-083-784-694038	Sequence 694038,
C 38	11	55.0	19	9	US-11-083-784-744106	Sequence 744106,
C 39	11	55.0	19	9	US-11-083-784-1071283	Sequence 1071283,
C 40	11	55.0	19	9	US-11-083-784-1104410	Sequence 1104410,
C 41	11	55.0	19	9	US-11-083-784-1104472	Sequence 1104472,
C 42	11	55.0	19	9	US-11-083-784-1279593	Sequence 1279593,
C 43	11	55.0	19	9	US-11-083-784-1280905	Sequence 1280905,
C 44	11	55.0	19	9	US-11-083-784-1286934	Sequence 1286934,
C 45	11	55.0	19	9	US-11-083-784-1286940	Sequence 1286940,

ALIGNMENTS

RESULT 1
US-11-101-244-619761/c
; Sequence 619761, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 619761
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-619761

Query Match 60.0%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTTGGTTGGGC 13
Db 19 CTTTGGTTGGGC 8

RESULT 2
US-11-101-244-619858/c
; Sequence 619858, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

us-10-671-074-172.oligo.rnpbn

Tue Jan 10 10:02:47 2006

```

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 619858
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-619858

Query Match      60.0%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 CTTTGGTTGGGC 13
      |||||
Db      19 CTTTGGTTGGGC 8

RESULT 3
US-11-101-244-1014343
; Sequence 1014343, Application US/11/101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1014343
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-1014343

Query Match      60.0%; Score 12; DB 8; Length 19;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      9 TGGGCAACACAT 20
      :|||
Db      6 UGGGCAACACAU 17

RESULT 4
US-11-101-244-1536666
; Sequence 1536666, Application US/11/101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1536666
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-1536666

Query Match      60.0%; Score 12; DB 8; Length 19;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTTTGGTTGGG 12
      ||::|||
Db      3 GCUUUGGUUGGG 14

RESULT 5
US-11-083-784-619761/c
; Sequence 619761, Application US/11/083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 619761
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-083-784-619761

Query Match      60.0%; Score 12; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 CTTTGGTTGGGC 13
      |||||
Db      19 CTTTGGTTGGGC 8

RESULT 6
US-11-083-784-619858/c
; Sequence 619858, Application US/11/083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
```



```
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 619858
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-619858
```

```
Query Match 60.0%; Score 12; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2 CTTTGGTTGGGC 13
Db 19 CTTTGGTTGGGC 8
```

```
RESULT 7
US-11-083-784-1014343
; Sequence 1014343, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1014343
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1014343
```

```
Query Match 60.0%; Score 12; DB 9; Length 19;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 9 TGGCAACACAT 20
Db 6 UGGCAACACAU 17
```

```
RESULT 8
US-11-083-784-1536666
; Sequence 1536666, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
```

```
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1536666
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1536666
```

```
Query Match 60.0%; Score 12; DB 9; Length 19;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GCTTTGGTTGGG 12
Db 3 GCUUUGUUGGG 14
```

```
RESULT 9
US-11-101-244-90162/c
; Sequence 90162, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 90162
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-90162
```

```
Query Match 55.0%; Score 11; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 4 TTGTTGGGCA 14
Db 16 TTGTTGGGCA 6
```

```
RESULT 10
US-11-101-244-204871
; Sequence 204871, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
```

<pre>; APPLICANT: Reynolds, Angela ; APPLICANT: Leake, Devin ; APPLICANT: Marshall, William ; APPLICANT: Scaringe, Stephen ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA ; FILE REFERENCE: 13499US ; CURRENT APPLICATION NUMBER: US/11/101,244 ; CURRENT FILING DATE: 2005-04-07 ; PRIOR APPLICATION NUMBER: 60/502,050 ; PRIOR FILING DATE: 2003-09-10 ; PRIOR APPLICATION NUMBER: 60/426,137 ; PRIOR FILING DATE: 2002-11-14 ; NUMBER OF SEQ ID NOS: 1591911 ; SOFTWARE: Proprietary ; SEQ ID NO 352435 ; LENGTH: 19 ; TYPE: RNA ; ORGANISM: Homo sapiens US-11-101-244-352435</pre>	<pre>Query Match 55.0%; Score 11; DB 8; Length 19; Best Local Similarity 90.9%; Pred. No. 8.2e+02; Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;</pre>	
<pre>QY 9 TGGGCAACACA 19 : Db 6 UGGGCAACACA 16</pre>	<pre>RESULT 13 US-11-101-244-580035/c ; Sequence 580035, Application US/11/101244 ; Publication No. US20050246794A1 ; GENERAL INFORMATION: ; APPLICANT: Dharmacon, Inc. ; APPLICANT: Khvorova, Anastasia ; APPLICANT: Reynolds, Angela ; APPLICANT: Leake, Devin ; APPLICANT: Marshall, William ; APPLICANT: Scaringe, Stephen ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA ; FILE REFERENCE: 13499US ; CURRENT APPLICATION NUMBER: US/11/101,244 ; CURRENT FILING DATE: 2005-04-07 ; PRIOR APPLICATION NUMBER: 60/502,050 ; PRIOR FILING DATE: 2003-09-10 ; PRIOR APPLICATION NUMBER: 60/426,137 ; PRIOR FILING DATE: 2002-11-14 ; NUMBER OF SEQ ID NOS: 1591911 ; SOFTWARE: Proprietary ; SEQ ID NO 580035 ; LENGTH: 19 ; TYPE: RNA ; ORGANISM: Homo sapiens US-11-101-244-580035</pre>	<pre>Query Match 55.0%; Score 11; DB 8; Length 19; Best Local Similarity 100.0%; Pred. No. 8.2e+02; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>
<pre>QY 2 CTTTGTGGG 12 Db 18 CTTTGTGGG 8</pre>	<pre>RESULT 14 US-11-101-244-676846/C ; Sequence 676846, Application US/11/101244 ; Publication No. US20050246794A1 ; GENERAL INFORMATION: ; APPLICANT: Dharmacon, Inc. ; APPLICANT: Khvorova, Anastasia ; APPLICANT: Reynolds, Angela</pre>	<pre>Query Match 55.0%; Score 11; DB 8; Length 19; Best Local Similarity 100.0%; Pred. No. 8.2e+02; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>

<pre>; APPLICANT: Khvorova, Anastasia ; APPLICANT: Reynolds, Angela ; APPLICANT: Leake, Devin ; APPLICANT: Marshall, William ; APPLICANT: Scaringe, Stephen ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA ; FILE REFERENCE: 13499US ; CURRENT APPLICATION NUMBER: US/11/101,244 ; CURRENT FILING DATE: 2005-04-07 ; PRIOR APPLICATION NUMBER: 60/502,050 ; PRIOR FILING DATE: 2003-09-10 ; PRIOR APPLICATION NUMBER: 60/426,137 ; PRIOR FILING DATE: 2002-11-14 ; NUMBER OF SEQ ID NOS: 1591911 ; SOFTWARE: Proprietary ; SEQ ID NO 204871 ; LENGTH: 19 ; TYPE: RNA ; ORGANISM: Homo sapiens US-11-101-244-204871</pre>	<pre>Query Match 55.0%; Score 11; DB 8; Length 19; Best Local Similarity 90.9%; Pred. No. 8.2e+02; Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;</pre>	
<pre>QY 9 TGGGCAACACA 19 : Db 8 UGGGCAACACA 18</pre>	<pre>RESULT 11 US-11-101-244-341693/c ; Sequence 341693, Application US/11/101244 ; Publication No. US20050246794A1 ; GENERAL INFORMATION: ; APPLICANT: Dharmacon, Inc. ; APPLICANT: Khvorova, Anastasia ; APPLICANT: Reynolds, Angela ; APPLICANT: Leake, Devin ; APPLICANT: Marshall, William ; APPLICANT: Scaringe, Stephen ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA ; FILE REFERENCE: 13499US ; CURRENT APPLICATION NUMBER: US/11/101,244 ; CURRENT FILING DATE: 2005-04-07 ; PRIOR APPLICATION NUMBER: 60/502,050 ; PRIOR FILING DATE: 2003-09-10 ; PRIOR APPLICATION NUMBER: 60/426,137 ; PRIOR FILING DATE: 2002-11-14 ; NUMBER OF SEQ ID NOS: 1591911 ; SOFTWARE: Proprietary ; SEQ ID NO 341693 ; LENGTH: 19 ; TYPE: RNA ; ORGANISM: Homo sapiens US-11-101-244-341693</pre>	<pre>Query Match 55.0%; Score 11; DB 8; Length 19; Best Local Similarity 100.0%; Pred. No. 8.2e+02; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>
<pre>QY 2 CTTTGTGGG 12 Db 18 CTTTGTGGG 8</pre>	<pre>RESULT 12 US-11-101-244-352435 ; Sequence 352435, Application US/11/101244 ; Publication No. US20050246794A1 ; GENERAL INFORMATION: ; APPLICANT: Dharmacon, Inc. ; APPLICANT: Khvorova, Anastasia</pre>	<pre>Query Match 55.0%; Score 11; DB 8; Length 19; Best Local Similarity 100.0%; Pred. No. 8.2e+02; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>

```
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 676846
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-676846
```

```
Query Match      55.0%; Score 11; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      8 TTGGGCAACAC 18
      |||||
Db      17 TTGGGCAACAC 7
```

```
RESULT 15
US-11-101-244-694038
; Sequence 694038, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 694038
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-694038
```

```
Query Match      55.0%; Score 11; DB 8; Length 19;
Best Local Similarity 54.5%; Pred. No. 8.2e+02;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GCTTTGGTTGG 11
      ||::||:
Db      8 GCUUUGGUUG 18
```

Search completed: January 10, 2006, 00:32:13
Job time : 321 secs

Handwritten text, possibly a signature or date, oriented vertically.

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 14:18:14 ; Search time 3642 Seconds
(without alignments)
256.931 Million cell updates/sec

Title: US-10-671-074-172

Perfect score: 20
Sequence: 1 gcttgggtgggaacacat 20

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12980

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database :

EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_est3:*
- 4: gb_hic:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_est7:*
- 9: gb_gse1:*
- 10: gb_gse2:*
- 11: gb_gse3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	9	45.0	19	AZ779085	2M0015B01
C 2	9	45.0	20	AZ448577	AZ448577 1M0246A22
C 3	8	40.0	13	CF543283	CF543283 S014680-0
C 4	8	40.0	14	DN987001	DN987001 MSU_28F_2
C 5	8	40.0	14	DN987019	DN987019 MSU_28F_2
C 6	8	40.0	14	DN987173	DN987173 MSU_2F_2
C 7	8	40.0	14	DN988472	DN988472 ZEBRA_28F
C 8	8	40.0	15	CA797315	CA797315 Cac BL_44
C 9	8	40.0	15	DN987063	DN987063 MSU_28F_2
C 10	8	40.0	16	AA936037	AA936037 nz53f05.8
C 11	8	40.0	16	DN987076	DN987076 MSU_2R_2
C 12	8	40.0	17	AW245605	AW245605 2827690.3
C 13	8	40.0	17	DN986605	DN986605 MSU_2F_2
C 14	8	40.0	18	DN986848	DN986848 MSU_28R_2
C 15	8	40.0	19	AW246512	AW246512 2821749.3
C 16	8	40.0	19	AZ344069	AZ344069 1M0077G21
C 17	8	40.0	19	AZ771432	AZ771432 1M0573003
C 18	8	40.0	19	AZ804081	AZ804081 2M0064118
C 19	8	40.0	20	AJ723010	AJ723010 AJ723010
C 20	8	40.0	20	BM395053	BM395053 50072-2.7
C 21	8	40.0	20	CO408232	CO408232 VRK436 Vi
C 22	8	40.0	20	AZ369118	AZ369118 1M0119106

C 23	8	40.0	20	9	AZ785716	AZ785716 2M0039F19
C 24	8	40.0	20	9	AZ789409	AZ789409 2M0037H11
C 25	7	35.0	11	5	BQ585171	BQ585171 S014222-0
C 26	7	35.0	12	10	AJ587358	AJ587358 Arabidops
C 27	7	35.0	13	1	AI016863	AI016863 ou27c10.x
C 28	7	35.0	13	5	BQ582420	BQ582420 E012207-0
C 29	7	35.0	15	10	AJ596116	AJ596116 Arabidops
C 30	7	35.0	15	10	AJ600925	AJ600925 Arabidops
C 31	7	35.0	16	1	AI154875	AI154875 ud80f04.r
C 32	7	35.0	16	8	DN988583	DN988583 ZEBRA_28R
C 33	7	35.0	17	1	AJ658902	AJ658902 AJ658902
C 34	7	35.0	17	1	BQ589968	BQ589968 S013719-0
C 35	7	35.0	17	5	BQ789989	BQ789989 hage005AB
C 36	7	35.0	18	5	BQ584776	BQ584776 E011673-0
C 37	7	35.0	18	10	AJ600524	AJ600524 Arabidops
C 38	7	35.0	19	1	AA977115	AA977115 Q24C08.s
C 39	7	35.0	19	1	AI281100	AI281100 QK57h11.x
C 40	7	35.0	19	1	AI688430	AI688430 wc89e09.x
C 41	7	35.0	19	1	AJ663023	AJ663023 AJ663023
C 42	7	35.0	19	6	CA794263	CA794263 Cac BL_12
C 43	7	35.0	19	8	CV998328	CV998328 lv46f09.b
C 44	7	35.0	19	9	AZ334192	AZ334192 1M0063A06
C 45	7	35.0	19	9	AZ339847	AZ339847 1M0071C06

ALIGNMENTS

RESULT 1
AZ779085/c

LOCUS
AZ779085 19 bp DNA linear GSS 16-FEB-2001

DEFINITION
2M0015B01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0015B01 F, genomic survey sequence.

ACCESSION
AZ779085

VERSION
AZ779085.1 GI:12909385

KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Bescorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0015 row: B column: 01
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0015B01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 45.0%; Score 9; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTGGTTGG 11
|||||
Db 14 TTTGGTTGG 6

RESULT 2

AZ448577/c

LOCUS

DEFINITION

1M0246A22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0246A22 F, genomic survey sequence.

ACCESSION

AZ448577

VERSION

GSS

KEYWORDS

Mus musculus (house mouse)

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0246 row: A column: 22

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0246A22"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

FEATURES

source

/note="Vector: pWD42nv; Purified genomic DNA from *M. musculus* C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 45.0%; Score 9; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTGGTTGG 11
|||||
Db 20 TTTGGTTGG 12

RESULT 3

CF543283

LOCUS

DEFINITION

S044680-024-030-D02-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone

024-030-D02 5-PRIME, mRNA sequence.

ACCESSION

CF543283

VERSION

EST

KEYWORDS

Beta vulgaris

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 13 Std Error: 0.00

Plate: 30 row: D column: 02

Seq primer: SP6.

Location/Qualifiers

1..13

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding line)"

/db_xref="GABI:936477"

/db_xref="taxon:161934"

/clone="024-030-D02"

/tissue_type="leaf"

/lab_host="EMDH10B"

/clone_lib="MP1Z-ADIS-024-leaf"

/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;

cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:

SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 40.0%; Score 8; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CAACACAT 20
|||||
Db 1 CAACACAT 8

RESULT 4
DN987001
LOCUS
DEFINITION
MSU 28F 2-II 04 MSU 28F 2-II 04 A04.ab1 linear EST 17-MAY-2005
subtracted cold acclimated cDNA library Cynodon dactylon cDNA clone
MSU 28F 2-II 04 MSU 28F 2-II 04 A04.ab1, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Cynodon dactylon (Bermuda grass)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Chloridoideae; Cynodonteae; Cynodon.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 14)
Melmaiee,K., Elavarthi,S. and Guenzi,A.C.
Identification of differentially expressed genes associated with
cold acclimation using suppression subtraction hybridization (SSH)
and cDNA microarrays
Unpublished (2005)

Contact: Guenzi AC
Dep. of Plant and Soil Sciences
Oklahoma State University
368 Agriculture Hall, Stillwater, OK 74078-6028, USA
Tel: 405-744-6028
Fax: 405 744 6039
Email: acg@mail.pss.okstate.edu
PCR Primers
FORWARD: M13 Forward
BACKWARD: M13 Reverse
Seq primer: M13 Forward.

FEATURES
source
1..14
/organism="Cynodon dactylon"
/mol_type="mRNA"
/cultivar="MSU"
/db_xref="taxon:28909"
/clone="MSU 28F 2-II 04 MSU 28F 2-II 04 A04.ab1"
/tissue_type="crown"
/lab_host="E. coli"
/clone_lib="Bermudagrass cv. MSU subtracted cold
acclimated cDNA library"
/note="Vector: Qiagen's pDrive; Messenger RNA was
extracted from control and cold acclimated bermudagrass
crown tissue at 2 and 28 days after acclimation and cDNA
library was constructed following Clontech PCR- select
cDNA subtraction procedure."

ORIGIN
Query Match 40.0%; Score 8; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGT 8
|||||
Db 6 GCTTTGGT 13

RESULT 5

DN987019

LOCUS

DEFINITION

MSU 28F 2-II 03 MSU 28F 2-II 03 G03.ab1 linear EST 17-MAY-2005

subtracted cold acclimated cDNA library Cynodon dactylon cDNA clone

MSU 28F 2-II 03 MSU 28F 2-II 03 G03.ab1, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Cynodon dactylon (Bermuda grass)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Chloridoideae; Cynodonteae; Cynodon.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 14)
Melmaiee,K., Elavarthi,S. and Guenzi,A.C.
Identification of differentially expressed genes associated with
cold acclimation using suppression subtraction hybridization (SSH)
and cDNA microarrays
Unpublished (2005)

Contact: Guenzi AC
Dep. of Plant and Soil Sciences
Oklahoma State University
368 Agriculture Hall, Stillwater, OK 74078-6028, USA
Tel: 405-744-6028
Fax: 405 744 6039
Email: acg@mail.pss.okstate.edu
PCR Primers
FORWARD: M13 Forward
BACKWARD: M13 Reverse
Seq primer: M13 Forward.

FEATURES

source

1..14
/organism="Cynodon dactylon"
/mol_type="mRNA"
/cultivar="MSU"
/db_xref="taxon:28909"
/clone="MSU 28F 2-II 03 MSU 28F 2-II 03 G03.ab1"
/tissue_type="crown"
/lab_host="E. coli"
/clone_lib="Bermudagrass cv. MSU subtracted cold
acclimated cDNA library"
/note="Vector: Qiagen's pDrive; Messenger RNA was
extracted from control and cold acclimated bermudagrass
crown tissue at 2 and 28 days after acclimation and cDNA
library was constructed following Clontech PCR- select
cDNA subtraction procedure."

ORIGIN

Query Match 40.0%; Score 8; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGT 8
|||||
Db 6 GCTTTGGT 13

RESULT 6

DN987173

LOCUS

DEFINITION

MSU 2F 2-II 05 MSU 2F 2-II 05 G08.ab1 linear EST 17-MAY-2005

subtracted cold acclimated cDNA library Cynodon dactylon cDNA clone

MSU 2F 2-II 05 MSU 2F 2-II 05 G08.ab1, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

Cynodon dactylon (Bermuda grass)

```

ORGANISM      Cynodon dactylon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Chloridoideae; Cynodonteae; Cynodon.
REFERENCE
AUTHORS      1 (bases 1 to 14)
TITLE        Identification of differentially expressed genes associated with
             cold acclimation using suppression subtraction hybridization (SSH)
             and cDNA microarrays
JOURNAL
COMMENT      Unpublished (2005)
             Contact: Guenzi AC
             Oklahoma State University
             368 Agriculture Hall, Stillwater, OK 74078-6028, USA
             Tel: 405-744-6028
             Fax: 405 744 6039
             Email: acg@mail.pss.okstate.edu
             PCR Primers
             FORWARD: M13 Forward
             BACKWARD: M13 Reverse
             Seq primer: M13 Forward.
FEATURES
source
1..14
/organism="Cynodon dactylon"
/mol_type="mRNA"
/cultivar="MSU"
/db_xref="taxon:28909"
/clone="MSU_2F_2-II_05_MSU_2F_2-II_05_G08.abi"
/tissue_type="crown"
/lab_host="E. coli"
/clone_lib="Bermudagrass cv. MSU substracted cold
acclimated cDNA library"
/note="Vector: Qiagen's pDrive; Messenger RNA was
extracted from control and cold acclimated bermudagrass
crown tissue at 2 and 28 days after acclimation and cDNA
library was constructed following Clontech PCR- select
cDNA subtraction procedure."
ORIGIN
Query Match      40.0%; Score 8; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 GCTTTGGT 8
        |||||
        6 GCTTTGGT 13
Db
RESULT 7
CA797315/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
Theobroma.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D.,
Retzel, E.R. and Jones, C.A.
Gene discovery and microarray analysis of cacao (Theobroma cacao
L.) varieties
JOURNAL
Planta 216 (2), 255-264 (2002)
PUBMED
12447539
COMMENT
Contact: Jones, Paul
Masterfoods
3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
Tel: +44 1664 416644
Email: Paul.Jones@eu.effem.com
Seq primer: T3.
FEATURES
source
1..15
/organism="Theobroma cacao"
/mol_type="mRNA"
/strain="Amelonado type"
/db_xref="taxon:3641"
/clone="Cac BL 4406"
/tissue_type="Mature leaf and mature bean"
/cell_type="Whole organ"
/dev_stage="maturity"
/lab_host="XL-1 Blue MRF"
/clone_lib="Cac BL (Bean and Leaf from Amelonado type
Cacao)"

```

```

Fax: 405 744 6039
Email: acg@mail.pss.okstate.edu
PCR Primers
FORWARD: M13 forward
BACKWARD: M13 Reverse
Seq primer: M13 Forward.
FEATURES
source
1..14
/organism="Cynodon dactylon"
/mol_type="mRNA"
/cultivar="Zebra"
/db_xref="taxon:28909"
/clone="ZEBRA_28F_2-II_08_ZEBRA_28F_2-II_08_F01.abi"
/tissue_type="crown"
/lab_host="E. coli"
/clone_lib="Bermudagrass line Zebra substracted cold
acclimated cDNA library"
/note="Vector: Qiagen's pDrive; Messenger RNA was
extracted from control and cold acclimated bermudagrass
crown tissue at 2 and 28 days after acclimation and cDNA
library was constructed following Clontech PCR- select
cDNA subtraction procedure."
ORIGIN
Query Match      40.0%; Score 8; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 GCTTTGGT 8
        |||||
        6 GCTTTGGT 13
Db
RESULT 8
CA797315/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
Theobroma.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D.,
Retzel, E.R. and Jones, C.A.
Gene discovery and microarray analysis of cacao (Theobroma cacao
L.) varieties
JOURNAL
Planta 216 (2), 255-264 (2002)
PUBMED
12447539
COMMENT
Contact: Jones, Paul
Masterfoods
3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
Tel: +44 1664 416644
Email: Paul.Jones@eu.effem.com
Seq primer: T3.
FEATURES
source
1..15
/organism="Theobroma cacao"
/mol_type="mRNA"
/strain="Amelonado type"
/db_xref="taxon:3641"
/clone="Cac BL 4406"
/tissue_type="Mature leaf and mature bean"
/cell_type="Whole organ"
/dev_stage="maturity"
/lab_host="XL-1 Blue MRF"
/clone_lib="Cac BL (Bean and Leaf from Amelonado type
Cacao)"

```



```

ORIGIN
/note="Vector: pBK-CMV; Bean and leaf tissue from an
Ameledonado type Cacao tree."

Query Match      40.0%; Score 8; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTGTTGG 11
Db 11 TTGTTGG 4

RESULT 9
DN987063
LOCUS
DEFINITION
MSU 28F 2-II_02_MSU_28F_2-II_02_B02.ab1 mRNA linear EST 17-MAY-2005
subtracted cold acclimated cDNA library Cynodon dactylon CDNA clone
MSU_28F_2-II_02_MSU_28F_2-II_02_B02.ab1, mRNA sequence.
DN987063
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Cynodon dactylon (Bermuda grass)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Chloridoideae; Cynodonteae; Cynodon.
1 (bases 1 to 15)
Melmaiee, K., Elavarthi, S. and Guenzi, A.C.
Identification of differentially expressed genes associated with
cold acclimation using suppression subtraction hybridization (SSH)
and cDNA microarrays
Unpublished (2005)
Contact: Guenzi AC
Dep. of Plant and Soil Sciences
Oklahoma State University
368 Agriculture Hall, Stillwater, OK 74078-6028, USA
Tel: 405-744-6028
Fax: 405 744 6039
Email: acg@mail.pss.okstate.edu
PCR Primers
FORWARD: M13 Forward
BACKWARD: M13 Reverse
Seq primer: M13 Forward.

FEATURES
source
1..15
/organism="Cynodon dactylon"
/mol_type="mRNA"
/cultivar="MSU"
/db_xref="taxon:28909"
/clone="MSU 28F_2-II_02_MSU_28F_2-II_02_B02.ab1"
/tissue_type="crown"
/lab_host="E. coli"
/clone_lib="Bermudagrass cv. MSU subtracted cold
acclimated cDNA library"
/note="Vector: Qiagen's pDrive; Messenger RNA was
extracted from control and cold acclimated bermudagrass
crown tissue at 2 and 28 days after acclimation and cDNA
library was constructed following Clontech PCR- select
cDNA subtraction procedure."

ORIGIN
Query Match      40.0%; Score 8; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGT 8
Db 7 GCTTTGGT 14

RESULT 10
AA936037

```

```

LOCUS
DEFINITION
AA936037      16 bp      mRNA      linear      EST 28-APR-1998
n253f05.s1 NCI_CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1291521
similar to TR:Q28150 Q28150 UNKNOWN PROTEIN ;, mRNA sequence.
AA936037
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
1 (bases 1 to 16)
Hominidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,
Rodrigo F. Chuquib, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES
source
1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1291521"
/sex="male"
/tissue_type="metastatic prostate bone lesion"
/lab_host="DH10B"
/clone_lib="NCI CGAP_Pr12"
/note="Vector: pAMP10; mRNA made from metastatic prostate
lesion of the bone, cDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel,
average insert size 600 bp. Library made by D. Krizman,
NIH."

ORIGIN
Query Match      40.0%; Score 8; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGGGCA 14
Db 3 GTTGGGCA 10

RESULT 11
DN987076
LOCUS
DEFINITION
MSU_2R_2-II_02_MSU_2R_2-II_02_H04.abi mRNA linear EST 17-MAY-2005
subtracted cold acclimated cDNA library Cynodon dactylon CDNA clone
MSU_2R_2-II_02_MSU_2R_2-II_02_H04.abi, mRNA sequence.
DN987076
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Cynodon dactylon (Bermuda grass)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Chloridoideae; Cynodonteae; Cynodon.
1 (bases 1 to 16)
Melmaiee, K., Elavarthi, S. and Guenzi, A.C.
Identification of differentially expressed genes associated with

```

JOURNAL COMMENT

cold acclimation using suppression subtraction hybridization (SSH) and cDNA microarrays
Unpublished (2005)
Contact: Guenzi AC
Dep. of Plant and Soil Sciences
Oklahoma State University
368 Agriculture Hall, Stillwater, OK 74078-6028, USA
Tel: 405-744-6028
Fax: 405 744 6039
Email: acg@mail.pss.okstate.edu

PCR Primers
FORWARD: M13 Forward
BACKWARD: M13 Reverse
Seq primer: M13 Forward.

FEATURES source

1. .16
/organism="Cynodon dactylon"
/mol_type="mRNA"
/cultivar="MSU"
/db_xref="taxon:28909"
/clone="MSU 2R 2-II_02_MSU 2R 2-II_02_H04.abi"
/tissue_type="Crown"
/lab_host="E. coli"
/clone_lib="Bermudagrass cv. MSU subtracted cold acclimated cDNA library"
/note="Vector: Qiagen's pDrive; Messenger RNA was extracted from control and cold acclimated bermudagrass crown tissue at 2 and 28 days after acclimation and cDNA library was constructed following Clontech PCR- select cDNA subtraction procedure."

ORIGIN

Query Match 40.0%; Score 8; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGT 8
|||||
Db 8 GCTTTGGT 15

RESULT 12
AW245605
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AW245605 17 bp mRNA linear EST 07-JAN-2000
2822690.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822690 3', mRNA sequence.
AW245605
AW245605.1 GI:6588598
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2822690.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ULNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 15 contiguous PHRED high quality bases following vector sequence. Very

JOURNAL COMMENT

Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LICM10 row: B column: 3
High quality sequence stop: 15.
Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2822690"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 40.0%; Score 8; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTTGGTTG 10
|||||
Db 8 TTTGGTTG 15

RESULT 13
DN986605
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

DN986605 17 bp mRNA linear EST 17-MAY-2005
MSU 2F 2-II_03_MSU 2F 2-II_03_E12.ab1 Bermudagrass cv. MSU subtracted cold acclimated cDNA library Cynodon dactylon cDNA clone
MSU 2F 2-II_03_MSU 2F 2-II_03_E12.ab1, mRNA sequence.
DN986605
DN986605.1 GI:66246432
EST.
Cynodon dactylon (Bermuda grass)
Cynodon dactylon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Chloridoideae; Cynodonteae; Cynodon.
1 (bases 1 to 17)
Melmaisee,K., Elavarthi,S. and Guenzi,A.C.
Identification of differentially expressed genes associated with cold acclimation using suppression subtraction hybridization (SSH) and cDNA microarrays
Unpublished (2005)
Contact: Guenzi AC
Dep. of Plant and Soil Sciences
Oklahoma State University
368 Agriculture Hall, Stillwater, OK 74078-6028, USA
Tel: 405-744-6028
Fax: 405 744 6039
Email: acg@mail.pss.okstate.edu
PCR Primers
FORWARD: M13 Forward
BACKWARD: M13 Reverse
Seq primer: M13 Forward.

FEATURES source

1. .17
/organism="Cynodon dactylon"
/mol_type="mRNA"
/cultivar="MSU"
/db_xref="taxon:28909"

```

/clone="MSU_2F_2-II_03_MSU_2F_2-II_03_E12.ab1"
/tissue_type="Crown"
/lab_host="E. coli"
/clone_lib="Bermudagrass cv. MSU subextracted cold
acclimated cDNA library"
/notes="Vector: Qiagen's pDrive; Messenger RNA was
extracted from control and cold acclimated bermudagrass
crown tissue at 2 and 28 days after acclimation and cDNA
library was constructed following Clontech PCR- select
cDNA subtraction procedure."

ORIGIN
Query Match          40.0%; Score 8; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGT 8
Db 9 GCTTTGGT 16

RESULT 14
DN986848
LOCUS
DEFINITION
MSU_28F_2-II_06_MSU_28F_2-II_06_H11.ab1 mRNA linear EST 17-MAY-2005
subextracted cold acclimated cDNA library Cynodon dactylon cDNA clone

ACCESSION
DN986848
VERSION
MSU_28F_2-II_06_MSU_28F_2-II_06_H11.ab1 mRNA sequence.
KEYWORDS
EST.
SOURCE
Cynodon dactylon (Bermuda grass)
ORGANISM
Cynodon dactylon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Chloridoideae; Cynodonteae; Cynodon.
1 (bases 1 to 18)
Melmaice, K., Elavarthi, S. and Guenzi, A.C.
Identification of differentially expressed genes associated with
cold acclimation using suppression subtraction hybridization (SSH)
and cDNA microarrays
Unpublished (2005)
JOURNAL
COMMENT
Contact: Guenzi AC
Dep. of Plant and Soil Sciences
Oklahoma State University
368 Agriculture Hall, Stillwater, OK 74078-6028, USA
Tel: 405-744-6028
Fax: 405 744 6039
Email: acg@mail.pss.okstate.edu
PCR Primers
FORWARD: M13 Forward
BACKWARD: M13 Reverse
Seq primer: M13 Forward.

FEATURES
source
1..18
/organism="Cynodon dactylon"
/mol_type="mRNA"
/cultivar="MSU"
/db_xref="taxon:28909"
/clone="MSU_28F_2-II_06_MSU_28F_2-II_06_H11.ab1"
/tissue_type="crown"
/lab_host="E. coli"
/clone_lib="Bermudagrass cv. MSU subextracted cold
acclimated cDNA library"
/notes="Vector: Qiagen's pDrive; Messenger RNA was
extracted from control and cold acclimated bermudagrass
crown tissue at 2 and 28 days after acclimation and cDNA
library was constructed following Clontech PCR- select
cDNA subtraction procedure."

ORIGIN
Query Match          40.0%; Score 8; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GCTTTGGT 8
Db 10 GCTTTGGT 17

RESULT 15
AW246512
LOCUS
DEFINITION
AW246512 19 bp mRNA linear EST 07-JAN-2000
2821749.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821749 3',
mRNA sequence.
ACCESSION
AW246512
VERSION
AW246512.1 GI:6589505
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 19)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2821749 5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross_match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 17
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 19 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LUCM7 row: J column: 22
High quality sequence stop: 17.
Location/Qualifiers
1..19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821749"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/notes="Organ: lung; Vector: pOTB7; Site: 1: XhoI; Site: 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

ORIGIN

```

Query Match          40.0%; Score 8; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTTGGTTG 10
Db 8 TTTGGTTG 15

```

us-10-671-074-172.oligo.rst

Tue Jan 10 10:02:47 2006

Search completed: January 10, 2006, 00:09:27
Job time : 3648 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 08:29:09 ; Search time 2157 Seconds
(without alignments)
527.060 Million cell updates/sec

Title: US-10-671-074-172

Perfect score: 20
Sequence: 1 gcttggttggaacacacat 20

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 5881141 seqs, 28421725653 residues

Word size : 0

Total number of hits satisfying chosen parameters: 911080

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_in.*
- 3: gb_env.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pr.*
- 9: gb_ro.*
- 10: gb_sts.*
- 11: gb_sy.*
- 12: gb_un.*
- 13: gb_vl.*
- 14: gb_htg.*
- 15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	55.0	16	ARI175685	ARI175685 Sequence
2	11	55.0	16	ARI195261	ARI195261 Sequence
3	11	55.0	16	AR222343	AR222343 Sequence
4	11	55.0	16	AR241462	AR241462 Sequence
5	11	55.0	16	BD014828	BD014828 Modulator
6	11	55.0	17	AX217789	AX217789 Sequence
7	11	55.0	17	AX217790	AX217790 Sequence
8	11	55.0	17	AX217791	AX217791 Sequence
9	11	55.0	17	AX217792	AX217792 Sequence
10	11	55.0	17	AX218164	AX218164 Sequence
11	11	55.0	18	AR096847	AR096847 Sequence
12	11	55.0	18	AR096848	AR096848 Sequence
13	11	55.0	18	BD088913	BD088913 A method
14	11	55.0	18	AR294810	AR294810 Sequence
15	11	55.0	18	AB068208	AB068208 Synthetic
16	11	55.0	19	AR035618	AR035618 Sequence
17	11	55.0	20	AR016229	AR016229 Sequence
18	11	55.0	20	AR060253	AR060253 Sequence

c	19	11	55.0	20	6	BD195406	BD195406 Male infe
c	20	11	55.0	20	6	AR300270	AR300270 Sequence
	21	11	55.0	20	6	AR315014	AR315014 Sequence
	22	11	55.0	20	6	AX590861	AX590861 Sequence
	23	10	50.0	16	6	CS114095	CS114095 Sequence
	24	10	50.0	16	6	AR009323	AR009323 Sequence
	25	10	50.0	17	6	AR060788	AR060788 Sequence
	26	10	50.0	17	6	BD203167	BD203167 Method an
	27	10	50.0	17	6	I31567	I31567 Sequence 19
c	28	10	50.0	17	6	ARI94070	ARI94070 Sequence
c	29	10	50.0	17	6	AR286059	AR286059 Sequence
c	30	10	50.0	17	6	AR398049	AR398049 Sequence
c	31	10	50.0	17	6	AX217788	AX217788 Sequence
c	32	10	50.0	17	6	AX723794	AX723794 Sequence
	33	10	50.0	18	6	AR096846	AR096846 Sequence
	34	10	50.0	18	6	ARI12302	ARI12302 Sequence
c	35	10	50.0	18	6	BD234639	BD234639 Thymidine
	36	10	50.0	18	6	CQ807628	CQ807628 Sequence
	37	10	50.0	18	6	CQ827865	CQ827865 Sequence
	38	10	50.0	18	6	CS038714	CS038714 Sequence
c	39	10	50.0	18	6	E26536	E26536 DTDST gene
c	40	10	50.0	18	6	AR230235	AR230235 Sequence
c	41	10	50.0	18	6	AX046415	AX046415 Sequence
	42	10	50.0	18	6	AX148881	AX148881 Sequence
	43	10	50.0	18	6	AX599288	AX599288 Sequence
	44	10	50.0	18	6	AX796154	AX796154 Sequence
	45	10	50.0	18	6	AX823114	AX823114 Sequence

ALIGNMENTS

RESULT 1	ARI175685	Sequence 85 from patent US 6309853.	16 bp	DNA	linear	PAT 17-DEC-2001
LOCUS	ARI175685					
DEFINITION	Sequence 85 from patent US 6309853.					
ACCESSION	ARI175685					
VERSION	ARI175685.1	GI:17916984				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 16)					
AUTHORS	Friedman, J.M., Zhang, Y. and Proenca, R.					
TITLE	Modulators of body weight, corresponding nucleic acids and proteins, and diagnostic and therapeutic uses thereof					
JOURNAL	Patent: US 6309853-A 85 30-OCT-2001;					
FEATURES	Location/Qualifiers					
source	1..16					
	/organism="unknown"					
	/mol_type="unassigned DNA"					
ORIGIN						
Query Match	55.0%;	Score 11;	DB 6;	Length 16;		
Best Local	Matches 11;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	9	TGGGCAACACA	19			
Db	1	TGGGCAACACA	11			
RESULT 2	ARI195261	Sequence 85 from patent US 6350730.	16 bp	DNA	linear	PAT 20-APR-2002
LOCUS	ARI195261					
DEFINITION	Sequence 85 from patent US 6350730.					
ACCESSION	ARI195261					
VERSION	ARI195261.1	GI:20244698				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 16)					

AUTHORS Friedman,J.M., Zhang,Y. and Proenca,R. OB polypeptides and modified forms as modulators of body weight JOURNAL Patent: US 6350730-A 85 26-FEB-2002; FEATURES Location/Qualifiers 1. .16 source /organism="unknown" /mol_type="unassigned DNA"		9 TGGGCAACACA 19 1 TGGGCAACACA 11	
ORIGIN		BD014828 16 bp DNA linear PAT 27-AUG-2002 Modulator of weight, corresponding nucleic acid and protein, and diagnosis and remedy utilization thereof.	
Query Match Best Local Similarity 100.0%; Pred. No. 1.2e+05; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy		BD014828 1 TGGGCAACACA 11	
Db			
RESULT 3 LOCUS DEFINITION AR222343 Sequence 85 from patent US 6429290. ACCESSION AR222343 VERSION AR222343.1 GI:23329828 KEYWORDS Unknown. SOURCE Unknown. ORGANISM Unclassified. REFERENCE 1 (bases 1 to 16) Friedman,J.M., Zhang,Y. and Proenca,R. AUTHORS OB polypeptides, modified forms and derivatives TITLE OB polypeptides, modified forms and derivatives JOURNAL Patent: US 6429290-A 85 06-AUG-2002; The Rockefeller University; NYC, NY FEATURES Location/Qualifiers 1. .16 source /organism="unknown" /mol_type="genomic DNA"		BD014828 16 bp DNA linear PAT 26-SEP-2002 Modulator of weight, corresponding nucleic acid and protein, and diagnosis and remedy utilization thereof.	
ORIGIN		BD014828 1 TGGGCAACACA 11	
Query Match Best Local Similarity 100.0%; Pred. No. 1.2e+05; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy		BD014828 1 TGGGCAACACA 11	
Db			
RESULT 4 LOCUS DEFINITION AR241462 Sequence 85 from patent US 6471956. ACCESSION AR241462 VERSION AR241462.1 GI:27287152 KEYWORDS Unknown. SOURCE Unknown. ORGANISM Unclassified. REFERENCE 1 (bases 1 to 16) Friedman,J.M., Zhang,Y. and Proenca,R. AUTHORS Ob polypeptides, modified forms and compositions thereto TITLE Ob polypeptides, modified forms and compositions thereto JOURNAL Patent: US 6471956-A 85 29-OCT-2002; The Rockefeller University; New York, NY FEATURES Location/Qualifiers 1. .16 source /organism="unknown" /mol_type="genomic DNA"		BD014828 16 bp DNA linear PAT 20-DEC-2002 Modulator of weight, corresponding nucleic acid and protein, and diagnosis and remedy utilization thereof.	
ORIGIN		BD014828 1 TGGGCAACACA 11	
Query Match Best Local Similarity 100.0%; Pred. No. 1.2e+05; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy		BD014828 1 TGGGCAACACA 11	
Db			
RESULT 5 LOCUS DEFINITION BD014828 Modulator of weight, corresponding nucleic acid and protein, and diagnosis and remedy utilization thereof. ACCESSION BD014828 VERSION BD014828.1 GI:22555635 KEYWORDS JP 2001157591-A/69. SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 16) Friedman,J.M., Zhang,Y., Proenca,R., Maffei,M., Halaas,J.L., Kajiwara,K. and Burley,S.K. AUTHORS Modulator of weight, corresponding nucleic acid and protein, and diagnosis and remedy utilization thereof TITLE Modulator of weight, corresponding nucleic acid and protein, and diagnosis and remedy utilization thereof JOURNAL Patent: JP 2001157591-A 69 12-JUN-2001; THE ROCKFELLER UNIVERSITY COMMENT OS Homo sapiens (human) PN JP 2001157591-A/69 PD 12-JUN-2001 PF 29-SEP-2000 JP 2000301496 PR 30-NOV-1994 US 08/347563,10-MAY-1995 US 08/439431 PR 07-JUN-1995 US 08/483211 PI JEFFRY M FRIEDMAN,YIVING ZHANG,RICARDO PROENCA,MARGHERITA PI MAFFEI PI JEFFRY L HALAAS,KETAN KAJIWARA,STEPHEN K BURLEY PC C12N15/09,A61K31/711,A61K38/00,A61K39/395,A61K45/00,A61K48/00, PC A61P3/04, PC A61P3/06,A61P3/10,A61P9/12,C07K14/47,C07K16/18,C12N1/19,C12N1/ PC C12N5/10,C12P21/02,C12P21/08,C12P21/08,C12O1/68,C12N1/19,C12R1/72, PC PC C12N5/10,C12P21/02,C12P21/08,C12N1/19,C12R1:19,C12N1/19,C12R1:72, PC (C12N1/19,C12R1:85), (C12N1/19,C12R1:19), (C12N1/19,C12R1:07), PC (C12N1/21,C12R1:46S), (C12N1/21,C12R1:38), (C12N5/10,C12R1:91), PC (C12P21/02,C12R1:19), (C12N15/00,A61K37/02,C12N5/00,C12N5/00, PC (C12N5/00,C12R1:91) CC Strandedness: Single; CC Topology: Linear; CC Marker AFM218x10 FH Key Location/Qualifiers FT source 1. .16 /organism="Homo sapiens (human)". FEATURES Location/Qualifiers 1. .16 source /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"		BD014828 16 bp DNA linear PAT 27-AUG-2002 Modulator of weight, corresponding nucleic acid and protein, and diagnosis and remedy utilization thereof.	
ORIGIN		BD014828 1 TGGGCAACACA 11	
Query Match Best Local Similarity 100.0%; Pred. No. 1.2e+05; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy		BD014828 1 TGGGCAACACA 11	
Db			
RESULT 6 LOCUS DEFINITION AX217789/c Sequence 3231 from Patent WO0159103. ACCESSION AX217789 VERSION AX217789.1 GI:15527850 KEYWORDS synthetic construct SOURCE		AX217789 17 bp RNA linear PAT 07-SEP-2001 Sequence 3231 from Patent WO0159103.	

ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., Mcswiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 3231 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
ORIGIN
Query Match 55.0%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred.No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CTTTGGTTGGG 12
|||||
Db 17 CTTTGGTTGGG 7
RESULT 7
AX217790/c
LOCUS AX217790 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 3232 from Patent WO0159103.
ACCESSION AX217790
VERSION AX217790.1 GI:15527851
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., Mcswiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 3232 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
ORIGIN
Query Match 55.0%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred.No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CTTTGGTTGGG 12
|||||
Db 16 CTTTGGTTGGG 6
RESULT 8
AX217791/c
LOCUS AX217791 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 3233 from Patent WO0159103.
ACCESSION AX217791
VERSION AX217791.1 GI:15527852
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., Mcswiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and

nogo gene expression
JOURNAL Patent: WO 0159103-A 3233 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
ORIGIN
Query Match 55.0%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred.No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CTTTGGTTGGG 12
|||||
Db 13 CTTTGGTTGGG 3
RESULT 9
AX217792/c
LOCUS AX217792 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 3234 from Patent WO0159103.
ACCESSION AX217792
VERSION AX217792.1 GI:15527853
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., Mcswiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 3234 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
ORIGIN
Query Match 55.0%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred.No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CTTTGGTTGGG 12
|||||
Db 12 CTTTGGTTGGG 2
RESULT 10
AX218164/c
LOCUS AX218164 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 3606 from Patent WO0159103.
ACCESSION AX218164
VERSION AX218164.1 GI:15528225
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., Mcswiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 3606 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
Location/Qualifiers

```
source
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

ORIGIN
Query Match          55.0%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 CTTGGTTGGG 12
    |||||
Db   15 CTTGGTTGGG 5

RESULT 11
AR096847          18 bp      DNA      linear      PAT 08-SEP-2000
LOCUS             Sequence 45 from patent US 6008344.
DEFINITION
ACCESSION AR096847
VERSION AR096847.1 GI:10026014
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match          55.0%; Score 11; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  5 TGGTTGGGCAA 15
    |||||
Db   3 TGGTTGGGCAA 13

RESULT 12
AR096848          18 bp      DNA      linear      PAT 08-SEP-2000
LOCUS             Sequence 46 from patent US 6008344.
DEFINITION
ACCESSION AR096848
VERSION AR096848.1 GI:10026016
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match          55.0%; Score 11; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  5 TGGTTGGGCAA 15
    |||||
Db   6 TGGTTGGGCAA 16

RESULT 13
BD088913/c        18 bp      DNA      linear      PAT 27-AUG-2002
LOCUS             A method of arraying genome clone.
DEFINITION
ACCESSION BD088913
VERSION BD088913.1 GI:22634523
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
GENOTECHS
PN JP 2001321190-A/1157
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001069285
PI EIICHI SOEDA
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
C12N15/00,
PC C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key
FT
FT source 1..18
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source
1..18
Location/Qualifiers
/organism="Artificial Sequence".

ORIGIN
Query Match          55.0%; Score 11; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  5 TGGTTGGGCAA 15
    |||||
Db   17 TGGTTGGGCAA 7

RESULT 14
AR294810          18 bp      DNA      linear      PAT 12-JUN-2003
LOCUS             Sequence 6545 from patent US 6537751.
DEFINITION
ACCESSION AR294810
VERSION AR294810.1 GI:31682094
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..18
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match          55.0%; Score 11; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  5 TGGTTGGGCAA 15
    |||||
Db   7 GTTGGGCAACA 17
```



```

Db      |||||
      4 GTTGGGCAACA 14

RESULT 15
AB068208/c
LOCUS   AB068208      18 bp    DNA        linear    SYN 21-MAY-2003
DEFINITION Synthetic construct DNA, forward primer for human STS sts-R45N15R-2
          at lp36.
ACCESSION AB068208
VERSION   AB068208.1  GI:15129012
KEYWORDS .
SOURCE    synthetic construct
          synthetic construct
          other sequences; artificial sequences.
REFERENCE
AUTHORS   1 Chen, Y. Z., Hayashi, Y., Wu, J. G., Takaoka, E., Maekawa, K.,
            Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,
            Morishashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Hori, A.
            and Soeda, E.
            2 A BAC-based STS-content map spanning a 35-Mb region of human
              chromosome 1p35-p36
              Genomics 74 (1), 55-70 (2001)
              11374902
REFERENCE 2 (bases 1 to 18)
AUTHORS   Direct Submission
            Hori, A.
TITLE     Submitted (04-AUG-2001) Akira Hori, Tohoku University School of
JOURNAL   Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
Tel: 81-22-717-8042, Fax: 81-22-717-8047)
FEATURES
source    Location/Qualifiers
            1..18
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
misc_feature 1..18
            /note="forward primer for human STS sts-R45N15R-2 at lp36
            sts-R45N15R-2 obtained from clones B23604, B190K13,
            B310A20, B359J17, B45N15, B63P6, B190K13, Human BAC
            library RPCI-11"

ORIGIN
Query Match      55.0%; Score 11; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 TGGTTGGGCAA 15
      |||||
Db      17 TGGTTGGGCAA 7

```

Search completed: January 9, 2006, 23:08:30
 Job time : 2162 secs

Copyright © 2000
by the American Psychological Association
0893-3200/00 \$12.00
DOI: 10.1037/0893-3200.20.1.1

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 08:21:43 ; Search time 477 Seconds
(without alignments)
279.442 Million cell updates

Perfect score: 20

Sequence: 1 gcttggttgggcaacacat 20

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2512440

Minimum DB seq length: 0

Maximum DB seq length: 9	Maximum DB seq length: 20
--------------------------	---------------------------

Post-processing: Listing first 45 summaries

Database : N Genesec 21:*

- ```
n1: geneseqm1980s:**
n2: geneseqm1990s:**
n3: geneseqm2000s:**
n4: geneseqm2001as:**
n5: geneseqm2002as:**
n6: geneseqm2002bs:**
n7: geneseqm2002cs:**
n8: geneseqm2003as:**
n9: geneseqm2003bs:**
n10: geneseqm2003cs:**
n11: geneseqm2003ds:**
n12: geneseqm2004as:**
n13: geneseqm2004bs:**
n14: geneseqm2005a:**
n15: geneseqm2005b:**
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID       | Description |
|------------|-------|-------------|--------|----|----------|-------------|
| 1          | 20    | 100.0       | 20     | 12 | ADN97882 | Monkey fo   |
| 2          | 20    | 100.0       | 20     | 12 | ADN40818 | Monkey fo   |
| 3          | 19    | 95.0        | 20     | 12 | ADN97750 | Human fox   |
| c 4        | 19    | 95.0        | 20     | 12 | ADN97828 | Human fox   |
| 5          | 19    | 95.0        | 20     | 12 | ADN40686 | Human for   |
| c 6        | 19    | 95.0        | 20     | 12 | ADN40784 | Human for   |
| 7          | 16    | 80.0        | 20     | 12 | ADN97751 | Human fox   |
| c 8        | 16    | 80.0        | 20     | 12 | ADN97829 | Human fox   |
| 9          | 16    | 80.0        | 20     | 12 | ADN40687 | Human for   |
| c 10       | 16    | 80.0        | 20     | 12 | ADN40765 | Human for   |
| c 11       | 14    | 70.0        | 20     | 12 | ADP76896 | Chimeric    |
| c 12       | 14    | 70.0        | 20     | 12 | ADP76326 | Chimeric    |
| c 13       | 14    | 70.0        | 20     | 12 | ADP76474 | Chimeric    |
| c 14       | 14    | 70.0        | 20     | 12 | ADP76236 | Chimeric    |
| c 15       | 14    | 70.0        | 20     | 12 | ADP76342 | Chimeric    |
| c 16       | 14    | 70.0        | 20     | 12 | ADP76371 | Chimeric    |
| c 17       | 14    | 70.0        | 20     | 12 | ADP76928 | Chimeric    |
| c 18       | 13    | 65.0        | 20     | 12 | ADP76645 | Chimeric    |
| c 19       | 13    | 65.0        | 20     | 12 | ADP77259 | Chimeric    |

## ALIGNMENTS

## RESULT 1

ADN97882  
ID ADN97882 standard; DNA; 20 BP.

AC ADN97882;

01-JUL-2004 (first entry)

XX Monkey foxhead box O1A sequence inhibitory oligo #1.

ss; cytostatic; antidiabetic; forehead box O1A inhibitor;  
KW forehead box O1A; hyperproliferative disorder; cancer; rhabdomyosarcoma;  
KW diabetes; H-ras gene; antisense; gene expression; primer.

XX  
OS  
Synthetic.XX  
PN W02004031350-A2XX  
PD  
15-APR-2004XX  
PP  
25-SEP-2003: 2003WC-IIS030352XX  
PR 26-SEP-2002: 2002US-00260203.

XX (AMGE-) AMGEN INC.  
PA (ISIS-) ISIS PHARM INC.

XX PI Dobie KW. Bhanot S. Veniant-Ellison M. Lindberg RA. Shutter JR:

XX  
DR  
WPI: 2004-330164/30.

xx New compounds, particularly antisense oligonucleotides, targeted to a  
PT nucleic acid molecule encoding forhead box O1A, useful for treating  
PT cancer, or type 2 diabetes.

Example 25: SEQ ID NO 172; 146pp; English.

The invention relates to a compound 8-80 nucleobases in length targeted to a nucleic acid molecule encoding forkhead box O1A, where the compound is at least 70% complementary to a nucleic acid molecule encoding forkhead box O1A and modulates expression of forkhead box O1A by at least 10%. The compound is useful for treating an animal having disease or

CC condition associated with forkhead box O1A, e.g. a hyperproliferative  
 CC disorder (cancer, preferably rhabdomyosarcoma), or type 2 diabetes. This  
 CC sequence corresponds to an oligonucleotide targeted to the monkey forkhead  
 CC box O1A genes in order to inhibit gene expression.

XX  
 SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.1;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGGCAACACAT 20  
 Db 1 GCTTTGGTTGGGCAACACAT 20

RESULT 2  
 ADN40818  
 ID ADN40818 standard; DNA; 20 BP.  
 XX  
 AC  
 ADN40818;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Monkey forkhead box O1A antisense oligonucleotide #1.  
 KW Monkey; forkhead box O1A; ss; antisense oligonucleotide;  
 KW phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety;  
 KW 5-methylcytosine; hyperproliferative disorder; cancer; rhabdomyosarcoma;  
 KW type 2 diabetes; cytostatic; antidiabetic.

XX  
 OS Primates.  
 XX  
 PN US2004097459-A1.  
 XX  
 PD 20-MAY-2004.  
 XX  
 PF 25-SEP-2003; 2003US-00671074.  
 XX  
 PR 26-SEP-2002; 2002US-00260203.  
 XX  
 PA (DOI/) DOBIE K W.  
 PA (BHANI) BHANOT S.  
 PA (VENI/) VENIANT-ELLISON M.  
 PA (LIND/) LINDBERG R A.  
 PA (SHUT/) SHUTTER J R.

XX  
 PI Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;  
 XX  
 XX WPI; 2004-389194/36.  
 XX  
 DR  
 XX New compounds, particularly antisense oligonucleotides, targeted to a  
 PT nucleic acid molecule encoding forkhead box O1A, useful for treating  
 PT cancer, or type 2 diabetes.

XX  
 PS Example 25; SEQ ID NO 172; 80pp; English.  
 XX  
 XX The invention relates to a compound targeted to a nucleic acid molecule  
 CC encoding the human forkhead box O1A polypeptide. The compound is an  
 CC antisense oligonucleotide that specifically hybridizes with the nucleic  
 CC acid and inhibits expression of the polypeptide. The antisense  
 CC oligonucleotide comprises at least one modified internucleoside linkage  
 CC i.e. a phosphorothioate linkage, at least one modified sugar moiety,  
 CC preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified  
 CC nucleobase comprising a 5-methylcytosine. The antisense compounds are  
 CC useful for modulating the expression of the human forkhead box O1A  
 CC polypeptide and in preparation of a composition for treating  
 CC hyperproliferative disorders, e.g. cancer, preferably rhabdomyosarcoma,  
 CC and type 2 diabetes. This sequence represents an antisense  
 CC oligonucleotide targeted to DNA encoding the monkey forkhead O1A  
 CC polypeptide of the invention.

XX Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.1;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTTGGTTGGGCAACACAT 20  
 Db 1 GCTTTGGTTGGGCAACACAT 20

RESULT 3  
 ADN97750  
 ID ADN97750 standard; DNA; 20 BP.  
 XX  
 AC  
 ADN97750;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Human forkhead box O1A sequence inhibitory oligo #23.  
 KW ss; cytostatic; antidiabetic; forkhead box O1A inhibitor;  
 KW forkhead box O1A; hyperproliferative disorder; cancer; rhabdomyosarcoma;  
 KW diabetes; H-ras gene; antisense; gene expression; primer.

XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_difference 1..20  
 FT /\*tag= b  
 FT /note= "sugar phosphate internucleotide linkages in the  
 FT backbone are replaced with a phosphorothioate  
 FT internucleotide linkages"  
 FT modified\_base 1..20  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "all C are 5'-methylcytidines"  
 FT modified\_base 1..5  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "nucleotides are 2'-methoxyethyl-nucleotides"  
 FT modified\_base 16..20  
 FT /\*tag= d  
 FT /mod\_base= OTHER  
 FT /note= "nucleotides are 2'-methoxyethyl-nucleotides"

WO2004031350-A2.

15-APR-2004.

25-SEP-2003; 2003WO-US030352.

26-SEP-2002; 2002US-00260203.

(AMGE-) AMGEN INC.  
 (ISIS-) ISIS PHARM INC.

Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;  
 WPI; 2004-330164/30.

New compounds, particularly antisense oligonucleotides, targeted to a  
 nucleic acid molecule encoding forkhead box O1A, useful for treating  
 cancer, or type 2 diabetes.

Claim 14; SEQ ID NO 40; 146pp; English.

The invention relates to a compound 8-80 nucleobases in length targeted  
 to a nucleic acid molecule encoding forkhead box O1A, where the compound  
 is at least 70% complementary to a nucleic acid molecule encoding  
 forkhead box O1A and modulates expression of forkhead box O1A by at least  
 10%. The compound is useful for treating an animal having a disease or  
 condition associated with forkhead box O1A, e.g. a hyperproliferative  
 disorder (cancer, preferably rhabdomyosarcoma), or type 2 diabetes. This

CC sequence corresponds to an oligonucleotide targeted to the human foxhead  
 CC box OIA genes in order to inhibit gene expression.  
 XX  
 SQ Sequence 20 BP; 4 A; 4 C; 5 G; 7 T; 0 U; 0 Other;  
 Query Match 95.0%; Score 19; DB 12; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.37; Indels 0; Gaps 0;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 CTTTGGTGGCAACACAT 20  
 |||||  
 Db 1 CTTTGGTGGCAACACAT 19  
 |||||  
 RESULT 4  
 ADN97828/c  
 ID ADN97828 standard; DNA; 20 BP.  
 XX  
 AC ADN97828;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Human foxhead box OIA gene target sequence #21.  
 XX  
 KW ss: cytostatic; antidiabetic; foxhead box OIA inhibitor;  
 KW foxhead box OIA; hyperproliferative disorder; cancer; rhabdomyosarcoma;  
 KW diabetes; H-ras gene; antisense; gene expression; primer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W02004031350-A2.  
 XX  
 PD 15-APR-2004.  
 XX  
 PF 25-SEP-2003; 2003WO-US030352.  
 XX  
 PR 26-SEP-2002; 2002US-00260203.  
 XX  
 PS (AMGE-) AMGEN INC.  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;  
 XX WPI; 2004-330164/30.  
 DR  
 XX  
 PT New compounds, particularly antisense oligonucleotides, targeted to a  
 PT nucleic acid molecule encoding foxhead box OIA, useful for treating  
 PT cancer, or type 2 diabetes.  
 XX  
 PS Example 18; SEQ ID NO 118; 146pp; English.  
 XX  
 CC The invention relates to a compound 8-80 nucleobases in length targeted  
 CC to a nucleic acid molecule encoding foxhead box OIA, where the compound  
 CC is at least 70% complementary to a nucleic acid molecule encoding  
 CC foxhead box OIA and modulates expression of foxhead box OIA by at least  
 CC 10%. The compound is useful for treating an animal having a disease or  
 CC condition associated with foxhead box OIA, e.g. a hyperproliferative  
 CC disorder (cancer, preferably rhabdomyosarcoma), or type 2 diabetes. This  
 CC sequence corresponds to a targeted sequence from the human foxhead box  
 CC OIA gene.  
 XX  
 SQ Sequence 20 BP; 7 A; 5 C; 4 G; 4 T; 0 U; 0 Other;  
 Query Match 95.0%; Score 19; DB 12; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.37; Indels 0; Gaps 0;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 CTTTGGTGGCAACACAT 20  
 |||||  
 Db 20 CTTTGGTGGCAACACAT 2  
 |||||  
 RESULT 5

ADN40686  
 ID ADN40686 standard; DNA; 20 BP.  
 XX  
 AC ADN40686;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Human foxhead box OIA DNA antisense oligonucleotide #23.  
 XX  
 KW Human; foxhead box OIA; ss; antisense oligonucleotide;  
 KW phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety;  
 KW 5-methylcytosine; hyperproliferative disorder; cancer; rhabdomyosarcoma;  
 KW type 2 diabetes; cytostatic; antidiabetic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004097459-A1.  
 XX  
 PD 20-MAY-2004.  
 XX  
 PF 25-SEP-2003; 2003US-00671074.  
 XX  
 PR 26-SEP-2002; 2002US-00260203.  
 XX  
 PA (DOBI/) DOBIE K W.  
 PA (BHAN/) BHANOT S.  
 PA (VENI/) VENIANT-ELLISON M.  
 PA (LIND/) LINDBERG R A.  
 PA (SHUT/) SHUTTER J R.  
 XX  
 PI Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;  
 XX WPI; 2004-389194/36.  
 DR  
 XX  
 PT New compounds, particularly antisense oligonucleotides, targeted to a  
 PT nucleic acid molecule encoding foxhead box OIA, useful for treating  
 PT cancer, or type 2 diabetes.  
 XX  
 PS Claim 14; SEQ ID NO 40; 80pp; English.  
 XX  
 CC The invention relates to a compound targeted to a nucleic acid molecule  
 CC encoding the human foxhead box OIA polypeptide. The compound is an  
 CC antisense oligonucleotide that specifically hybridizes with the nucleic  
 CC acid and inhibits expression of the polypeptide. The antisense  
 CC oligonucleotide comprises at least one modified internucleoside linkage,  
 CC i.e. a phosphorothioate linkage, at least one modified sugar moiety,  
 CC preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified  
 CC nucleobase comprising a 5-methylcytosine. The antisense compounds are  
 CC useful for modulating the expression of the human foxhead box OIA  
 CC polypeptide and in preparation of a composition for treating  
 CC hyperproliferative disorders, e.g. cancer, preferably rhabdomyosarcoma,  
 CC and type 2 diabetes. This sequence represents an antisense  
 CC oligonucleotide targeted to DNA encoding the human foxhead OIA  
 CC polypeptide of the invention.  
 XX  
 SQ Sequence 20 BP; 4 A; 4 C; 5 G; 7 T; 0 U; 0 Other;  
 Query Match 95.0%; Score 19; DB 12; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.37; Indels 0; Gaps 0;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 CTTTGGTGGCAACACAT 20  
 |||||  
 Db 1 CTTTGGTGGCAACACAT 19  
 |||||  
 RESULT 6  
 ADN40764/c  
 ID ADN40764 standard; DNA; 20 BP.  
 XX  
 AC ADN40764;  
 XX  
 DT 12-AUG-2004 (first entry)

Tue Jan 10 10:02:46 2006

```
XX DE Human forkhead box O1A DNA antisense oligonucleotide target region #21.
XX FT Human; forkhead box O1A; ss; antisense oligonucleotide;
XX FT phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety;
KW KW 5-methylcytosine; hyperproliferative disorder; cancer; rhabdomyosarcoma;
KW KW type 2 diabetes; cytostatic; antidiabetic.
XX OS Homo sapiens.
XX PN US2004097459-A1.
XX PD 20-MAY-2004.
XX PF 25-SEP-2003; 2003US-00671074.
XX PR 26-SEP-2002; 2002US-00260203.
XX PA (DOBIE/) DOBIE K W.
XX PA (BHANT/) BHANT S.
XX PA (VENIANT/) VENIANT-ELLISON M.
XX PA (LIND/) LINDBERG R A.
XX PA (SHUT/) SHUTTER J R.
XX PI Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;
XX WI WIPI; 2004-389194/36.
XX FT New compounds, particularly antisense oligonucleotides, targeted to a
XX FT nucleic acid molecule encoding forkhead box O1A, useful for treating
XX FT cancer, or type 2 diabetes.
XX PS Example 18; SEQ ID NO 118; 80pp; English.
XX CC The invention relates to a compound targeted to a nucleic acid molecule
XX CC encoding the human forkhead box O1A polypeptide. The compound is an
XX CC antisense oligonucleotide that specifically hybridizes with the nucleic
XX CC acid and inhibits expression of the polypeptide. The antisense
XX CC oligonucleotide comprises at least one modified internucleoside linkage
XX CC i.e. a phosphorothioate linkage, at least one modified sugar moiety,
XX CC preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified
XX CC nucleobase comprising a 5-methylcytosine. The antisense compounds are
XX CC useful for modulating the expression of the human forkhead box O1A
XX CC polypeptide and in preparation of a composition for treating
XX CC hyperproliferative disorders, e.g. cancer, preferably rhabdomyosarcoma,
XX CC and type 2 diabetes. This sequence represents a human forkhead O1A DNA
XX CC antisense oligonucleotide target region of the invention.
XX SQ Sequence 20 BP; 7 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 95.0%; Score 19; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTTGGTTGGGCAACACAT 20
Db 20 CTTTGGTTGGGCAACACAT 2
|||||
|||||

RESULT 7
ADN97751
ID ADN97751 standard; DNA; 20 BP.
AC ADN97751;
XX 01-JUL-2004 (first entry)
XX Human forkhead box O1A sequence inhibitory oligo #24.
XX ss; cytostatic; antidiabetic; forkhead box O1A inhibitor;
KW KW forkhead box O1A; hyperproliferative disorder; cancer; rhabdomyosarcoma;
KW KW diabetes; H-ras gene; antisense; gene expression; primer.
XX

XX OS Synthetic.
XX FT Key misc_difference 1..20
XX FT /tag= b
XX FT /note= "sugar phosphate internucleotide linkages in the
XX FT backbone are replaced with a phosphorothioate
XX FT internucleotide linkages"
XX FT modified_base 1..20
XX FT /tag= c
XX FT /mod_base= OTHER
XX FT /note= "all C are 5'-methylcytidines"
XX FT modified_base 1..5
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "nucleotides are 2'-methoxyethyl-nucleotides"
XX FT modified_base 16..20
XX FT /tag= d
XX FT /mod_base= OTHER
XX FT /note= "nucleotides are 2'-methoxyethyl-nucleotides"
XX PN WO2004031350-A2.
XX PD 15-APR-2004.
XX PR 25-SEP-2003; 2003WO-US030352.
XX PR 26-SEP-2002; 2002US-00260203.
XX PA (AMGE-) AMGEN INC.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;
XX WI WIPI; 2004-330164/30.
XX FT New compounds, particularly antisense oligonucleotides, targeted to a
XX FT nucleic acid molecule encoding forkhead box O1A, useful for treating
XX FT cancer, or type 2 diabetes.
XX PS Claim 14; SEQ ID NO 41; 146pp; English.
XX CC The invention relates to a compound 8-80 nucleobases in length targeted
XX CC to a nucleic acid molecule encoding forkhead box O1A, where the compound
XX CC is at least 70% complementary to a nucleic acid molecule encoding
XX CC forkhead box O1A and modulates expression of forkhead box O1A by at least
XX CC 10%. The compound is useful for treating an animal having a disease or
XX CC condition associated with forkhead box O1A, e.g. a hyperproliferative
XX CC disorder (cancer, preferably rhabdomyosarcoma), or type 2 diabetes. This
XX CC sequence corresponds to an oligonucleotide targeted to the human forkhead
XX CC box O1A genes in order to inhibit gene expression.
XX SQ Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTTGGCAAC 16
Db 5 GCTTTGGTTGGCAAC 20
|||||
|||||

RESULT 8
ADN97829/c
ID ADN97829 standard; DNA; 20 BP.
XX AC ADN97829;
XX 01-JUL-2004 (first entry)
XX Human forkhead box O1A gene target sequence #22.
XX DE Human forkhead box O1A gene target sequence #22.
XX
```

KW ss; cytostatic; antidiabetic; foxhead box O1A inhibitor;  
 KW forkhead box O1A; hyperproliferative disorder; cancer; rhabdomyosarcoma;  
 KW diabetes; H-ras gene; antisense; gene expression; primer.  
 OS Homo sapiens.  
 XX WO2004031350-A2.  
 XX 15-APR-2004.  
 XX 25-SEP-2003; 2003WO-US030352.  
 XX 26-SEP-2002; 2002US-00260203.  
 XX (AMGE-) AMGEN INC.  
 PA (ISIS-) ISIS PHARM INC.  
 XX Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;  
 XX WPI; 2004-330164/30.  
 XX New compounds, particularly antisense oligonucleotides, targeted to a  
 PT nucleic acid molecule encoding forkhead box O1A, useful for treating  
 PT cancer, or type 2 diabetes.  
 XX Example 18; SEQ ID NO 119; 146pp; English.  
 XX The invention relates to a compound 8-80 nucleobases in length targeted  
 CC to a nucleic acid molecule encoding forkhead box O1A, where the compound  
 CC is at least 70% complementary to a nucleic acid molecule encoding  
 CC forkhead box O1A and modulates expression of forkhead box O1A by at least  
 CC 10%. The compound is useful for treating an animal having a disease or  
 CC condition associated with forkhead box O1A, e.g. a hyperproliferative  
 CC disorder (cancer, preferably rhabdomyosarcoma), or type 2 diabetes. This  
 CC sequence corresponds to a targeted sequence from the human foxhead box  
 CC O1A gene.  
 XX  
 SQ Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;  
 Query Match 80.0%; Score 16; DB 12; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 GCTTTGGTTGGGCAAC 16  
 Db 16 GCTTTGGTTGGGCAAC 1  
 RESULT 9  
 ADN40687  
 ID ADN40687 standard; DNA; 20 BP.  
 XX  
 AC ADN40687;  
 XX  
 DT 12-AUG-2004 (first entry)  
 DE Human forkhead box O1A DNA antisense oligonucleotide #24.  
 XX  
 DE Human; forkhead box O1A; ss; antisense oligonucleotide;  
 KW phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety;  
 KW 5-methylcytosine; hyperproliferative disorder; cancer; rhabdomyosarcoma;  
 KW type 2 diabetes; cytostatic; antidiabetic.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2004097459-A1.  
 PN 20-MAY-2004.  
 XX  
 XX 25-SEP-2003; 2003US-00671074.  
 PF  
 XX 26-SEP-2002; 2002US-00260203.  
 PR  
 XX

PA (DOBI/) DOBIE K W.  
 PA (BHAN/) BHANOT S.  
 PA (VENI/) VENIANT-ELLISON M.  
 PA (LIND/) LINDBERG R A.  
 PA (SHUT/) SHUTTER J R.  
 XX  
 PI Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;  
 XX WPI; 2004-389194/36.  
 XX New compounds, particularly antisense oligonucleotides, targeted to a  
 PT nucleic acid molecule encoding forkhead box O1A, useful for treating  
 PT cancer, or type 2 diabetes.  
 XX Claim 14; SEQ ID NO 41; 80pp; English.  
 XX The invention relates to a compound targeted to a nucleic acid molecule  
 CC encoding the human forkhead box O1A polypeptide. The compound is an  
 CC antisense oligonucleotide that specifically hybridizes with the nucleic  
 CC acid and inhibits expression of the polypeptide. The antisense  
 CC oligonucleotide comprises at least one modified internucleoside linkage,  
 CC i.e. a phosphorothioate linkage, at least one modified sugar moiety,  
 CC preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified  
 CC nucleobase comprising a 5-methylcytosine. The antisense compounds are  
 CC useful for modulating the expression of the human forkhead box O1A  
 CC polypeptide and in preparation of a composition for treating  
 CC hyperproliferative disorders, e.g. cancer, preferably rhabdomyosarcoma,  
 CC and type 2 diabetes. This sequence represents an antisense  
 CC oligonucleotide targeted to DNA encoding the human forkhead O1A  
 CC polypeptide of the invention.  
 XX  
 SQ Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;  
 Query Match 80.0%; Score 16; DB 12; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 GCTTTGGTTGGGCAAC 16  
 Db 5 GCTTTGGTTGGGCAAC 20  
 RESULT 10  
 ADN40765/c  
 ID ADN40765 standard; DNA; 20 BP.  
 XX  
 AC ADN40765;  
 XX  
 DT 12-AUG-2004 (first entry)  
 DE Human forkhead box O1A DNA antisense oligonucleotide target region #22.  
 XX  
 DE Human; forkhead box O1A; ss; antisense oligonucleotide;  
 KW phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety;  
 KW 5-methylcytosine; hyperproliferative disorder; cancer; rhabdomyosarcoma;  
 KW type 2 diabetes; cytostatic; antidiabetic.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2004097459-A1.  
 PN 20-MAY-2004.  
 XX  
 XX 25-SEP-2003; 2003US-00671074.  
 PF  
 XX 26-SEP-2002; 2002US-00260203.  
 PR  
 XX (DOBI/) DOBIE K W.  
 PA (BHAN/) BHANOT S.  
 PA (VENI/) VENIANT-ELLISON M.  
 PA (LIND/) LINDBERG R A.  
 PA (SHUT/) SHUTTER J R.  
 XX

PI Dobie KW, Bhanot S, Veniant-Ellison M, Lindberg RA, Shutter JR;  
XX WPI; 2004-389194/36.  
XX New compounds, particularly antisense oligonucleotides, targeted to a  
PT nucleic acid molecule encoding forkhead box O1A, useful for treating  
PT cancer, or type 2 diabetes.  
XX  
XX Example 18; SEQ ID NO 119; 80pp; English.  
XX The invention relates to a compound targeted to a nucleic acid molecule  
CC encoding the human forkhead box O1A polypeptide. The compound is an  
CC antisense oligonucleotide that specifically hybridizes with the nucleic  
CC acid and inhibits expression of the polypeptide. The antisense  
CC oligonucleotide comprises at least one modified internucleoside linkage  
CC i.e. a phosphorothioate linkage, at least one modified sugar moiety,  
CC preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified  
CC nucleobase comprising a 5-methylcytosine. The antisense compounds are  
CC useful for modulating the expression of the human forkhead box O1A  
CC polypeptide and in preparation of a composition for treating  
CC hyperproliferative disorders, e.g. cancer, preferably rhabdomyosarcoma,  
CC and type 2 diabetes. This sequence represents a human forkhead O1A DNA  
CC antisense oligonucleotide target region of the invention.  
XX  
XX Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;  
SQ

Query Match 80.0%; Score 16; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTGGTGGGCAAC 16  
|||||  
Db 16 GCTTTGGTGGGCAAC 1

RESULT 11  
ADP76896/c  
ID ADP76896 standard; DNA; 20 BP.  
XX  
XX ADP76896;  
AC  
XX 12-AUG-2004 (first entry)  
DT  
XX Chimeric phosphorothioate oligonucleotide #695.  
DE  
XX GFAT; Antidiabetic; Cardiant;  
XX Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;  
KW reperfusion; ss.  
KW  
XX Synthetic.  
OS  
XX Key Location/Qualifiers  
FH modified\_base 1..4  
FT /\*tag= a  
FT /mod\_base= other  
FT /note= "2-methoxyethyl wing"  
FT modified\_base 17..20  
FT /\*tag= b  
FT /mod\_base= other  
FT /note= "2-methoxyethyl wing"  
FT  
FT  
XX WO2004035763-A2.  
XX  
XX 29-APR-2004.  
PD  
XX 02-OCT-2003; 2003WO-US033332.  
XX  
XX 17-OCT-2002; 2002US-0419268P.  
XX  
XX (PHAA ) PHARMACIA CORP.  
XX Broschat KO, Crosby SD;  
XX WPI; 2004-348453/32.  
XX

DR WPI; 2004-348453/32.  
XX New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase  
PT (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,  
PT ischemia/reperfusion injury.  
XX  
XX Claim 4; SEQ ID NO 695; 175pp; English.  
XX  
XX The present invention relates to a compound which specifically hybridizes  
CC with a nucleic acid molecule encoding GFAT, and inhibits the expression  
CC of GFAT. Specifically claimed are antisense oligonucleotides capable of  
CC modulating the expression of GFAT, and which comprise any of the 3063  
CC sequences of 20 base pairs, given in the specification. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with GFAT, such as a disease or condition, e.g. diabetes, a  
CC cardiovascular or neurological disorder, ischemia/reperfusion injury.  
CC They are also useful in research and diagnostics for modulating the  
CC expression of GFAT. The present sequence represents a chimeric  
CC phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these  
CC oligonucleotides inhibit human GFAT expression.  
XX  
XX Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;  
SQ

Query Match 70.0%; Score 14; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGGGCAACACAT 20  
|||||  
Db 14 GTTGGGCAACACAT 1

RESULT 12  
ADP76326/c  
ID ADP76326 standard; DNA; 20 BP.  
XX  
XX ADP76326;  
AC  
XX 12-AUG-2004 (first entry)  
DT  
XX Chimeric phosphorothioate oligonucleotide #125.  
DE  
XX GFAT; Antidiabetic; Cardiant;  
KW Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;  
KW reperfusion; ss.  
KW  
XX Synthetic.  
OS  
XX Key Location/Qualifiers  
FH modified\_base 1..4  
FT /\*tag= a  
FT /mod\_base= other  
FT /note= "2-methoxyethyl wing"  
FT modified\_base 17..20  
FT /\*tag= b  
FT /mod\_base= other  
FT /note= "2-methoxyethyl wing"  
FT  
FT  
XX WO2004035763-A2.  
XX  
XX 29-APR-2004.  
PD  
XX 02-OCT-2003; 2003WO-US033332.  
XX  
XX 17-OCT-2002; 2002US-0419268P.  
XX  
XX (PHAA ) PHARMACIA CORP.  
XX Broschat KO, Crosby SD;  
XX WPI; 2004-348453/32.  
XX



PT New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase  
PT (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,  
PT ischemia/reperfusion injury.  
XX  
XX  
PS Claim 4; SEQ ID NO 125; 175pp; English.  
XX  
CC The present invention relates to a compound which specifically hybridizes  
CC with a nucleic acid molecule encoding GFAT, and inhibits the expression  
CC of GFAT. Specifically claimed are antisense oligonucleotides capable of  
CC modulating the expression of GFAT, and which comprise any of the 3063  
CC sequences of 20 base pairs, given in the specification. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with GFAT, such as a disease or condition, e.g. diabetes, a  
CC cardiovascular or neurological disorder, ischemia/reperfusion injury.  
CC They are also useful in research and diagnostics for modulating the  
CC expression of GFAT. The present sequence represents a chimeric  
CC phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these  
CC oligonucleotides inhibit human GFAT expression.  
XX  
SQ Sequence 20 BP; 3 A; 7 C; 3 G; 7 T; 0 U; 0 Other;  
Query Match 70.0%; Score 14; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 GTTGGGCAACACAT 20  
Db 20 GTTGGGCAACACAT 7  
RESULT 13  
ADP76474/c  
ID ADP76474 standard; DNA; 20 BP.  
XX  
AC ADP76474;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Chimeric phosphorothioate oligonucleotide #273.  
XX  
KW GFAT; Antidiabetic; Cardiant;  
KW Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;  
KW reperfusion; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1...4  
FT /tag= a  
FT /mod\_base= other  
FT /note= "2-methoxyethyl wing"  
FT modified\_base 17..20  
FT /tag= b  
FT /mod\_base= other  
FT /note= "2-methoxyethyl wing"  
XX  
PN WO2004035763-A2.  
XX  
PD 29-APR-2004.  
XX  
PF 02-OCT-2003; 2003WO-US033332.  
XX  
PR 17-OCT-2002; 2002US-0419268P.  
XX  
PA (PHAA ) PHARMACIA CORP.  
XX  
PI Broschat KO, Crosby SD;  
XX  
DR WPI; 2004-348453/32.  
XX  
PT New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase

PT (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,  
PT ischemia/reperfusion injury.  
XX  
XX  
PS Claim 4; SEQ ID NO 273; 175pp; English.  
XX  
CC The present invention relates to a compound which specifically hybridizes  
CC with a nucleic acid molecule encoding GFAT, and inhibits the expression  
CC of GFAT. Specifically claimed are antisense oligonucleotides capable of  
CC modulating the expression of GFAT, and which comprise any of the 3063  
CC sequences of 20 base pairs, given in the specification. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with GFAT, such as a disease or condition, e.g. diabetes, a  
CC cardiovascular or neurological disorder, ischemia/reperfusion injury.  
CC They are also useful in research and diagnostics for modulating the  
CC expression of GFAT. The present sequence represents a chimeric  
CC phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these  
CC oligonucleotides inhibit human GFAT expression.  
XX  
SQ Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;  
Query Match 70.0%; Score 14; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 GTTGGGCAACACAT 20  
Db 16 GTTGGGCAACACAT 3  
RESULT 14  
ADP76296/c  
ID ADP76296 standard; DNA; 20 BP.  
XX  
AC ADP76296;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Chimeric phosphorothioate oligonucleotide #95.  
XX  
KW GFAT; Antidiabetic; Cardiant;  
KW Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;  
KW reperfusion; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..4  
FT /tag= a  
FT /mod\_base= other  
FT /note= "2-methoxyethyl wing"  
FT modified\_base 17..20  
FT /tag= b  
FT /mod\_base= other  
FT /note= "2-methoxyethyl wing"  
XX  
PN WO2004035763-A2.  
XX  
PD 29-APR-2004.  
XX  
PF 02-OCT-2003; 2003WO-US033332.  
XX  
PR 17-OCT-2002; 2002US-0419268P.  
XX  
PA (PHAA ) PHARMACIA CORP.  
XX  
PI Broschat KO, Crosby SD;  
XX  
DR WPI; 2004-348453/32.  
XX  
PT New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase  
PT (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,  
PT ischemia/reperfusion injury.

XX Claim 4; SEQ ID NO 95; 175pp; English.

XX The present invention relates to a compound which specifically hybridizes

CC with a nucleic acid molecule encoding GFAT, and inhibits the expression

CC of GFAT. Specifically claimed are antisense oligonucleotides capable of

CC modulating the expression of GFAT, and which comprise any of the 3063

CC sequences of 20 base pairs, given in the specification. The compound,

CC composition and methods are useful for treating a disease or condition,

CC associated with GFAT, such as a disease or condition, e.g. diabetes, a

CC cardiovascular or neurological disorder, ischemia/reperfusion injury.

CC They are also useful in research and diagnostics for modulating the

CC expression of GFAT. The present sequence represents a chimeric

CC phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these

CC oligonucleotides inhibit human GFAT expression.

XX Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

SQ

Query Match 70.0%; Score 14; DB 12; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGGGCAACACAT 20

Db 18 GTTGGGCAACACAT 5

|||||

RESULT 15

ADP76342/c

ID ADP76342 standard; DNA; 20 BP.

AC ADP76342;

XX 12-AUG-2004 (first entry)

XX Chimeric phosphorothioate oligonucleotide #141.

XX GFAT; Antidiabetic; Cardiant;

KW Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;

KW reperfusion; ss.

XX Synthetic.

XX Key Location/Qualifiers

FH modified\_base 1..4

FT /\*tag= a

FT /mod\_base= other

FT /note= "2-methoxyethyl wing"

FT modified\_base 17..20

FT /\*tag= b

FT /mod\_base= other

FT /note= "2-methoxyethyl wing"

XX WO2004035763-A2.

XX 29-APR-2004.

XX 02-OCT-2003; 2003WO-US033332.

XX 17-OCT-2002; 2002US-0419268P.

XX (PHAA ) PHARMACIA CORP.

XX Broschat KO, Crosby SD;

PI WPI; 2004-348453/32.

XX New compounds, particularly antisense oligonucleotides targeted to a

PT nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase

PT (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,

XX ischemia/reperfusion injury.

XX Claim 4; SEQ ID NO 141; 175pp; English.

XX The present invention relates to a compound which specifically hybridizes

CC with a nucleic acid molecule encoding GFAT, and inhibits the expression

CC of GFAT. Specifically claimed are antisense oligonucleotides capable of

CC modulating the expression of GFAT, and which comprise any of the 3063

CC sequences of 20 base pairs, given in the specification. The compound,

CC composition and methods are useful for treating a disease or condition,

CC associated with GFAT, such as a disease or condition, e.g. diabetes, a

CC cardiovascular or neurological disorder, ischemia/reperfusion injury.

CC They are also useful in research and diagnostics for modulating the

CC expression of GFAT. The present sequence represents a chimeric

CC phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these

CC oligonucleotides inhibit human GFAT expression.

XX Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

SQ

Query Match 70.0%; Score 14; DB 12; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGGGCAACACAT 20

Db 19 GTTGGGCAACACAT 6

|||||

Search completed: January 9, 2006, 22:32:18

Job time : 483 secs